

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 23, 2004, 05:01:30 ; Search time 9940 Seconds
(without alignments)
11376.456 Million cell updates/sec

Title: US-10-618-839-1
Perfect score: 2609
Sequence: 1 gctgatacacagttctgtc.....aaaaaaaaaaaaaaaaaaaaa 2609

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl.*

- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vl.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
- 19: em_mu.*
- 20: em_om.*
- 21: em_or.*
- 22: em_ov.*
- 23: em_pat.*
- 24: em_ph.*
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- 27: em_sts.*
- 28: em_un.*
- 29: em_vi.*
- 30: em_htg_hum.*
- 31: em_htg_inv.*
- 32: em_htg_other.*
- 33: em_htg_mus.*
- 34: em_htg_pln.*
- 35: em_htg_rod.*
- 36: em_htg_mam.*
- 37: em_htg_vrt.*
- 38: em_sy.*
- 39: em_htgo_hum.*
- 40: em_htgo_mus.*
- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	2605	99.8	2609	6	AR399401	AR399401 Sequence
2	2605	99.8	2609	6	AX351497	AX351497 Sequence
3	2605	99.8	2609	6	AX676981	AX676981 Sequence
4	2605	99.8	2609	9	AF127763	AF127763 Homo sapi
5	2593	99.4	2608	6	AX367290	AX367290 Sequence
6	1820.2	69.8	1881	6	AX367207	AX367207 Sequence
7	1820.2	69.8	1881	9	AF166327	AF166327 Homo sapi
8	1516.2	58.1	1734	9	AF166328	AF166328 Homo sapi
9	1384.6	53.1	1548	9	HSA438989	HSA438989 Homo sapi
10	1307.8	50.1	1692	10	AF533979	AF533979 Mus muscu
11	1305	50.0	2577	6	AR399418	AR399418 Sequence
12	1305	50.0	2577	10	AF152963	AF152963 Rattus no
13	1182.8	45.3	2619	6	AR399430	AR399430 Sequence
14	1036.6	39.7	1353	10	AV174116	AV174116 Mus muscu
15	630.6	24.2	66424	9	HS146H21	Z83819 Human DNA s
16	588.4	22.6	1713	10	RNO259590	AJ295950 Rattus no
17	588.4	22.6	1714	10	MMU43384	U43384 Mus musculu
18	582.4	22.3	1857	4	AF323788	AF323788 Oryctolag
19	582	22.3	1713	10	AF298656	AF298656 Rattus no
20	582	22.3	4324	6	AX281787	AX281787 Sequence
21	582	22.3	4339	9	BC032720	BC032720 Homo sapi
22	579.4	22.2	4267	6	AR380834	AR380834 Sequence
23	579.4	22.2	4267	9	HSXCGD	X04011 Human mRNA
24	578.6	22.2	1778	4	AF036097	AF036097 Bos tauru
25	573.6	22.0	1713	4	AF411135	AF411135 Bison bis
26	560	21.5	3527	5	BC054624	BC054624 Danio rer
27	559.4	21.4	1755	4	AB034192	AB034192 Tursiops
28	551.6	21.1	658	6	AX367208	AX367208 Sequence
29	551.6	21.1	658	6	AX676982	AX676982 Sequence
30	551.6	21.1	658	9	AF166326	AF166326 Homo sapi
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32	521.2	20.0	2044	6	AR399402	AR399402 Sequence
33	521.2	20.0	2044	6	AX590295	AX590295 Sequence
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35	478.8	18.4	558	6	AX340272	AX340272 Sequence
36	474.8	18.2	1792	10	AY182377	AY182377 Mus muscu
37	468.6	18.0	491	6	AX351480	AX351480 Sequence
38	460.6	17.7	573	6	AX341610	AX341610 Sequence
39	446.2	17.1	449	6	AX341527	AX341527 Sequence
40	426.4	16.3	1558	4	SSU02476	U02476 Sus scrofa
41	405.4	15.5	428	6	BD226778	BD226778 A novel m
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43	385.8	14.8	517	4	OC271882	AF271882 Oryctolag
44	362.2	13.9	381	6	AX351286	AX351286 Sequence
45	331	12.7	331	6	AX247173	AX247173 Sequence

ALIGNMENTS

RESULT 1
AR399401
LOCUS AR399401 2609 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 1 from patent US 6620603.
ACCESSION AR399401
VERSION AR399401.1 GI:40141268
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2609)
AUTHORS Lambeth,J.D., Griendling,K.K., Lassegue,B.P., Arnold,R.S. and Cheng,G.
TITLE Human mitogenic oxidase
JOURNAL Patent: US 6620603-A 1 16-SEP-2003;

FEATURES		Location/Qualifiers	
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QY	1	GCTGATAGCACAGCTCTGTGTCACAGAGGAGGCGGAATAAATCTATTATCCACAGGAA	60
Db	1	GCTGATAGCACAGCTCTGTGTCACAGAGGAGGCGGAATAAATCTATTATCCACAGGAA	60
QY	61	CTCTTGGGGTAGGTGTGTGTTTTTTCATCTTAAAGGCTCACAGACCCTGCGCTGGACAA	120
Db	61	CTCTTGGGGTAGGTGTGTGTTTTTTCATCTTAAAGGCTCACAGACCCTGCGCTGGACAA	120
QY	121	ATGTTCCATCTCGAAGGACCTCTCCAGATCCGGATTCGGATCTTCCGCTTGCCTA	180
Db	121	ATGTTCCATCTCGAAGGACCTCTCCAGATCCGGATTCGGATCTTCCGCTTGCCTA	180
QY	181	GAAAGGCTCCAAACCACTCTTGACAAATGGGAACTGGGTGTTAAACCACTGTTTTCAG	240
Db	181	GAAAGGCTCCAAACCACTCTTGACAAATGGGAACTGGGTGTTAAACCACTGTTTTCAG	240
QY	241	TTTGTGTTCTGTGTTGTTAGGCTGAATCTTTTCTGTTTGTGGATGCTTCTCTGA	300
Db	241	TTTGTGTTCTGTGTTGTTAGGCTGAATCTTTTCTGTTTGTGGATGCTTCTCTGA	300
QY	301	AATATGAGAGCGCGACAAATCTACTACAGAAATATCTTGGTCAACATTTGGCCT	360
Db	301	AATATGAGAGCGCGACAAATCTACTACAGAAATATCTTGGTCAACATTTGGCCT	360
QY	361	GTCCCGAGGCTGTGCTCTGTCTGTAATTTTAAACAGCAGCTGATCCTGCTTCTGTG	420
Db	361	GTCCCGAGGCTGTGCTCTGTCTGTAATTTTAAACAGCAGCTGATCCTGCTTCTGTG	420
QY	421	GTCCGAATCTGTGCTCTCTGAGGGCACCTGTCTCAATTTTGCAGCGGCACACTGAGAA	480
Db	421	GTCCGAATCTGTGCTCTCTGAGGGCACCTGTCTCAATTTTGCAGCGGCACACTGAGAA	480
QY	481	AGCAATTTGATCACACCTCACTTCCACAGCTGGTGGCTATATGATCTGCTACATA	540
Db	481	AGCAATTTGATCACACCTCACTTCCACAGCTGGTGGCTATATGATCTGCTACATA	540
QY	541	CAGCTATTACATCATTTGCACACCTGTTTAACTTTGACTGCTATAGCAGAACCGCAGG	600
Db	541	CAGCTATTACATCATTTGCACACCTGTTTAACTTTGACTGCTATAGCAGAACCGCAGG	600
QY	601	CCAAGATGGCTCCCTTGGCTCATTCTCCAGCTTATCTCATGATGAGAAAAGGGGG	660
Db	601	CCAAGATGGCTCCCTTGGCTCATTCTCCAGCTTATCTCATGATGAGAAAAGGGGG	660
QY	661	GTTCTTGGCTTAAATCCATCCAGTCCCGAAACACGACAGTGGAGTATGTCACATTTCACCA	720
Db	661	GTTCTTGGCTTAAATCCATCCAGTCCCGAAACACGACAGTGGAGTATGTCACATTTCACCA	720
QY	721	GGCTTGGCTGTCTCACTGGAGTGCATGACAAATAGCCTTTGATTTCTCATGGTAACTTCAG	780
Db	721	GGCTTGGCTGTCTCACTGGAGTGCATGACAAATAGCCTTTGATTTCTCATGGTAACTTCAG	780
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Db	781	CTACTGATTCATCCGAGAGTATTTTGAAGTCTTCTGGTATPACTCACCACTTTTAA	840
QY	841	TCTTCTATATCTTGGCTTAGGANTTCAACGGCATTTGGTGAATTTGTCGGGGTCAAAACAG	900
Db	841	TCTTCTATATCTTGGCTTAGGANTTCAACGGCATTTGGTGAATTTGTCGGGGTCAAAACAG	900
QY	901	AGGAGACATGAATAGAGATCACTCGGAAAGTGTGCAGAGTCTTTTGAGATGTGGGATG	960
Db	901	AGGAGACATGAATAGAGATCACTCGGAAAGTGTGCAGAGTCTTTTGAGATGTGGGATG	960

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Db	961	ATCGTGACTCCCACTGTAGGCGCCCTTAAGTTTGAAGGGCATCCCTCTGATGTCTTGAAGT	1020
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Db	1021	GGATCTTGCACGGTCATTCTTTATATCTGTGAAGGATCTCCGGTTTTCACGCTCCG	1080
QY	1081	AGCAGAAGGTTCGATTACCAAGGTTGTTATGACCCATCCAAAGTTTTCGAATTCGAGA	1140
Db	1081	AGCAGAAGGTTCGATTACCAAGGTTGTTATGACCCATCCAAAGTTTTCGAATTCGAGA	1140
QY	1141	TGAACAAGCGTGTCTTTCAGATGGAAGTGGGCGAGTATATCTTTGTATATTCGCCCTCAA	1200
Db	1141	TGAACAAGCGTGTGTCTTTCAGATGGAAGTGGGCGAGTATATCTTTGTATATTCGCCCTCAA	1200
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Db	1201	TCTCTCTCTGNAATGGCATCTTTTACCTTTCACCTCTCTGCTCCAGAGGAAAGTTTCTTCT	1260
QY	1261	CCATTCTATATCCAGCAGCAGGGGACTGGAAGAAATCTCATPAAGGGCTTTTCGAACAAC	1320
Db	1261	CCATTCTATATCCAGCAGCAGGGGACTGGAAGAAATCTCATPAAGGGCTTTTCGAACAAC	1320
QY	1321	AATATTACCAATTTCCAGATTTGAAGTGGTGGTCCCTTTGGCAGCAGCAGTGGAGATG	1380
Db	1321	AATATTACCAATTTCCAGATTTGAAGTGGTGGTCCCTTTGGCAGCAGCAGTGGAGATG	1380
QY	1381	TTTTTCCAGTATGAAGTGGCTGTGCTGTTGGAGCAGGAATTTGGGTTCACCCCTTTTGTCT	1440
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Db	1441	CTATCTTGAATTCATCTGGTACAAATCCAGTGTGCAGACCAACCACTTCAAAACAAAA	1500
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QY	1561	TGACTTCCCTGGAAACAGGAGATGGAGAAATAGGCAAAAGTGGGTTTCTTAAACTACGCTC	1620
Db	1561	TGACTTCCCTGGAAACAGGAGATGGAGAAATAGGCAAAAGTGGGTTTCTTAAACTACGCTC	1620
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Db	1801	GCCTCGGACTTTGGCAAGAGCCTCGGCAAAATGCTGTACCGATATTCAGTCTGATC	1860
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Db	1861	CTAGAAAGTTTCAATTTCTACTTCAACAAAGAAATTTTGGTATATAGGAATAAGGACCG	1920
QY	1921	TAAATCTGCAATTTGTCTCTTTTGTATCTTCAATTAATGAGTTATAGGAATAAGGACGTA	1980
Db	1921	TAAATCTGCAATTTGTCTCTTTTGTATCTTCAATTAATGAGTTATAGGAATAAGGACGTA	1980
QY	1981	TCTGCAATTTGTCTCTTTTGTATCTTCAATTAATGAGTTATAGGAATAAGGACGTA	2040
Db	1981	TCTGCAATTTGTCTCTTTTGTATCTTCAATTAATGAGTTATAGGAATAAGGACGTA	2040

QY	2041	CACCTTAGGATAAGAAATGGCTCTCAAGCCTTGACTCCCTGGTATTCTTTTGGATTG	2100
Db	2041	CACCTTAGGATAAGAAATGGCTCTCAAGCCTTGACTCCCTGGTATTCTTTTGGATTG	2100
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QY	2221	CCATGACTGTAGCAAGGCTTGATAGCAGAAATTTGGTGGTTCANAATTATACAACTAATC	2280
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Db	2581	AAAAAAAAAAAAAAAAAAAAAAAAAAAAA	2609
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DEFINITION	Sequence 244 from Patent WO0196390.	linear	PAT 06-FEB-2002
ACCESSION	AX351497		
VERSION	AX351497.1	GI:18616842	
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	Jiang, Y., Hepler, W. T., Clapper, J. D., Wang, A. and Secrist, H.		
TITLE	Compositions and methods for the therapy and diagnosis of colon cancer		
JOURNAL	Patent: WO 0196390-A 244 20-DEC-2001;		
FEATURES	CORIXA CORPORATION (US)		
source	Location/Qualifiers		
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QY	121	ATGTTTCCATTCCTGAAGGACCTCTCCAGAAATCGGATTCCTGAATCTTCCCTGTTGCTTA	180
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Db	181	GAAAGGCTCCAAACCACTCTTGACAAATGGGAACTGGGTGGTTAAACCACTGGTTTCAG	240
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Db	241	TTTGTCTTCTGTTTGTGTTAGGCTGAATGTTTTCTGTTTGTGGATGCTTCTCTCA	300
QY	301	ATATGAGAGGCCGACAAATACTACTACACAAGAAAAATCTTGGGTCAACATTTGGCT	360
Db	301	ATATGAGAGGCCGACAAATACTACTACACAAGAAAAATCTTGGGTCAACATTTGGCT	360
QY	361	GTGCCGAGCGTCTGCTCTCTGCTTGAATTTTAAACAGCAGCGTGAATCTGCTTCTGCTGT	420
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Db	541	CAGCTAATTCACATCAATTCACACCTGTTTAACTTTGACTGTAGTAGAGAGCCGACAGG	600
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QY	901	AGGAGACATGAATGAGAGTCACTCTCGCAAGTGTGAGAGTCTTTTGAATGTTGGGATG	960
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Db	1141		TGAACAAGCGTGGCTTCAGCATGGAAGTGGGCGAGTATATCTTTGTTAAATTTGCCCTCAA	1200
Qy	1201	TCTCTCTCTCGAATGGCATCTTTTACTTTTGACCTCTGCTCCAGAGGAAGATTTCTTCT		1260
Db	1201	TCTCTCTCTCGAATGGCATCTTTTACTTTTGACCTCTGCTCCAGAGGAAGATTTCTTCT		1260
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Db	1801	GCCCTCGGACTTTGGCAAGAGCTGGCAAAATGCTGTCAACGATATCCAGTCTGGATC	1860	
Qy	1861	CTAGAAAGGTTCAATTTCTACTTCAACAAAGAAAATTTTGGAGTTATAGGAATAGGACGG	1920	
Db	1861	CTAGAAAGGTTCAATTTCTACTTCAACAAAGAAAATTTTGGAGTTATAGGAATAGGACGG	1920	
Qy	1921	TAATCTGCATTTTGTCTCTTTTGTATCTTCAATTTAGTATTTAGGAATTAAGGACGGTAA	1980	
Db	1921	TAATCTGCATTTTGTCTCTTTTGTATCTTCAATTTAGTATTTAGGAATTAAGGACGGTAA	1980	
Qy	1981	TCTGCATTTTGTCTCTTTTGTATCTTCAATTTAGTATTTAGGTTTTCAGTCTGANCAGT	2040	
Db	1981	TCTGCATTTTGTCTCTTTTGTATCTTCAATTTAGTATTTAGGTTTTCAGTCTGANCAGT	2040	
Qy	2041	CACTTTATAGGATAAGAAATGTGCTCTCAAGCGCTTGAATTTTGGTATTTTGGTATG	2100	
Db	2041	CACTTTATAGGATAAGAAATGTGCTCTCAAGCGCTTGAATTTTGGTATTTTGGTATG	2100	
Qy	2101	CATTCAACTTGGTATCTTGTAGCTTCAGCAACTTAAAGAACTTTGAAGTTCTTAAAGTTCT	2160	
Db	2101	CATTCAACTTGGTATCTTGTAGCTTCAGCAACTTAAAGAACTTTGAAGTTCTTAAAGTTCT	2160	
Qy	2161	GAANTTCTTAAAGCCCATGGATCTTTCTCAGAAAAATAACTCTGTAATCTTTCTGGACAG	2220	
Db	2161	GAANTTCTTAAAGCCCATGGATCTTTCTCAGAAAAATAACTCTGTAATCTTTCTGGACAG	2220	
Qy	2221	CCATGACTGTAGCAGGCTTGATAGCAGAAAGTTTGGTGGTTCANAATTTACAACTTAATC	2280	

2221	CCATGACTGTAGCAGGCTTGATAGCAGAAAGTTTGGTGGTTCANAATTTACAACTTAATC	2280
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2461	ATCCCATATACCAACACAGTGCATGTTTACTGTCACTTTTGTATATGTTTATTCACG	2520
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RESULT 3

AX676981	LOCUS	AX676981	2609 bp	DNA	linear	PAT 27-MAR-2003
AX676981	DEFINITION	Sequence 174 from Patent WO02103028.				
AX676981	ACCESSION					
AX676981.1	VERSION	GI:29334517				
	KEYWORDS	Homo sapiens (human)				
	SOURCE	Homo sapiens				
	ORGANISM	Homo sapiens				
	REFERENCE	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutharia; Primates; Catarrhini; Hominidae; Homo.				
	AUTHORS	Baranova, A.V., Yankovsky, N.K., Kozlov, A.P., Lobashev, A.V. and Krukovskaya, L.L.				
	TITLE	In silico screening for phenotype-associated expressed sequences				
	JOURNAL	Patent: WO 02103028-A 174 27-DEC-2002; Biomedical Center (RU)				
	FEATURES	Location/Qualifiers				
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		/db_xref="taxon:9606"				

ORIGIN

Query Match	99.8%;	Score 2605;	DB 6;	Length 2609;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 2609;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	1	GCTGATAGCAGCAGTCTCTGCTCCAGAGAAAGGAGCGCGAATAAACTTATTTCATTCACAGGAA	60
Db	1	GCTGATAGCAGCAGTCTCTGCTCCAGAGAGGAGGCGGAAATAAACTTATTTCATTCACAGGAA	60
Qy	61	CTCTTGGGGTAGTGTGTGTTTTCATCTTTAAAGGCTCACAGACCCCTGGCTGGACAA	120
Db	61	CTCTTGGGGTAGTGTGTGTTTTCATCTTTAAAGGCTCACAGACCCCTGGCTGGACAA	120
Qy	121	ATGTTCCATTCCTGAGGACCTCTCCAGATCCGAGATTCGTGAATCTTCCCTGTTGCCTA	180
Db	121	ATGTTCCATTCCTGAGGACCTCTCCAGATCCGAGATTCGTGAATCTTCCCTGTTGCCTA	180
Qy	181	GAAGGGCTCCAAACACCTCTTTCGACAAATCGGAAACTGGGTGGTTAACCACTGGTTTCAG	240
Db	181	GAAGGGCTCCAAACACCTCTTTCGACAAATCGGAAACTGGGTGGTTAACCACTGGTTTCAG	240
Qy	241	TTTTGTTTCTGCTGTTGGTTAGGCTGAATGTTTTCTCTGTTTGTGGATGCTTCTCTGA	300

Db 241 TTTTGTCTGTGTTGTTGGTCTAGGCTGAATGTTTCTGTGTTGTTGGATGCCTCTCTGA 300
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QY 1021 GGATCCTTGCACCGGTCACTCTTTATATCTGTGAAGGATCTCCGGTTTACCGCTCCC 1080
Db 1021 GGATCCTTGCACCGGTCACTCTTTATATCTGTGAAGGATCTCCGGTTTACCGCTCCC 1080
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QY 1321 AATATTACCAATTTCCAGGATTTGAAGTGGATGTGCTTCTTGGCACAGCAGTGAAGT 1380
Db 1321 AATATTACCAATTTCCAGGATTTGAAGTGGATGTGCTTCTTGGCACAGCAGTGAAGT 1380

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RESULT 5

AX367290

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

Location/Qualifiers

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ORIGIN

Query Match

Best Local Similarity

Matches 2608;

Conservative

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Mismatches

0;

Indels

1;

Gaps

1;

QY 1

1

1

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Db	301	AATATGAGAAGCGGCAAAATACTACTACACAGAAATAATCCTTGGGTCAACATTGGCCT	360	1381	TTTTTCCAGPATGAGTGGCTGTCTGGTTGGAGCAGGAATTTGGGGTCAACCCCTTTGCTT	1440
QY	361	GTGCGGAGCGTCTGCTCTCTGCTTGAATTTTAAACAGCAGCGTGTATCCTGCTTCTGTGT	420	1441	CTATCTTGAATTCATCTGGTACAAATTCACAGTGTGCACACCAACCTCAAAACAAAA	1500
Db	361	GTGCGGAGCGTCTGCTCTCTGCTTGAATTTTAAACAGCAGCGTGTATCCTGCTTCTGTGT	420	1441	CTATCTTGAATTCATCTGGTACAAATTCACAGTGTGCACACCAACCTCAAAACAAAA	1500
QY	421	GTGCGAATCTGTGTCTCTGCTTGGGGGCACTGTGCTCATTTTGCAGCGGACACTGAGAA	480	1501	AGATCTATTCTACTGATCTCAGGGAGACAGGTGCTTTTCTCTGGTTTCAACAACCTGT	1560
Db	421	GTGCGAATCTGTGTCTCTGCTTGGGGGCACTGTGCTCATTTTGCAGCGGACACTGAGAA	480	1501	AGATCTATTCTACTGATCTCAGGGAGACAGGTGCTTTTCTCTGGTTTCAACAACCTGT	1560
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Db	841	TCTTCTATATCTTGGCTTAGGATTCACGGCATTTGGTGAATTTGTCGGGGTCAAAACAG	900	1921	TAATCTGCAATTTGTCTCTTTGTATCTTTCAGTAAATTGAGTTATAGGAATAAGGACGGTAA	1980
QY	901	AGGAGACATGAATGAGAGTCACTCTCGCAAGTGTGCAGAGTCTTTTGGAGATGGGATG	960	1981	TCTGCAATTTGTCTCTTTGTATCTTTCAGTAAATTACCTGTGCTCCTCAGGTTTTCAGT	2040
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RESULT 7
AF166327
LOCUS 1881 bp mRNA linear PRI 06-JAN-2000
DEFINITION Homo sapiens NADPH oxidase homolog 1 long form (NOHL) mRNA,
alternatively spliced, complete cds.
ACCESSION AF166327
VERSION AF166327.1 GI:6672077
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1881)
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Banfi, B., Maturana, A., Jaconi, S., Arnaudeau, S., Laforge, T.,
Sinha, B., Ligeti, E., Demareux, N. and Krause, K.H.
TITLE A mammalian H+ channel generated through alternative splicing of
the NADPH oxidase homolog NOH-1
JOURNAL Science 287 (5450), 138-142 (2000)
MEDLINE 20082959
PUBMED 10615049
REFERENCE 2 (bases 1 to 1881)
Banfi, B., Maturana, A., Jaconi, S., Arnaudeau, S., Laforge, T.,
Sinha, B., Ligeti, E., Demareux, N. and Krause, K.H.
AUTHORS Direct Submission
TITLE Submitted (08-JUL-1999) Dept. of Geriatrics, Geneva University
JOURNAL Hospitals, 2, ch. du Petit-Bel-Air, Chene-Bourg CH-1225,
Switzerland

FEATURES
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RESULT 8
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 DEFINITION Homo sapiens NADPH oxidase homolog 1 long form variant (NOH1) mRNA,
 alternatively spliced, complete cds.
 ACCESSION AF166328
 VERSION AF166328.1 GI:6672079
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1734)
 Banfi, B., Maturana, A., Jaconi, S., Arnaudeau, S., Laforge, T.,
 Sinha, B., Ligeti, B., Demaurex, N. and Krause, K.H.
 A mammalian H+ channel generated through alternative splicing of
 the NADPH oxidase homolog NOH-1
 Science 287 (5450), 138-142 (2000)
 20082959
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 2 (bases 1 to 1734)
 Banfi, B., Maturana, A., Jaconi, S., Arnaudeau, S., Laforge, T.,
 Sinha, B., Ligeti, B., Demaurex, N. and Krause, K.H.
 Direct Submission
 Submitted (08-JUL-1999) Dept. of Geriatrics, Geneva University
 Hospitals, 2, ch. du Petit-Bel-Air, Chene-Bourg CH-1225,
 Switzerland

FEATURES

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 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
 AUTHORS Haenze, J.
 TITLE NOX-1 is expressed in pulmonary cells
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1548)
 AUTHORS Haenze, J.
 TITLE Direct Submission
 JOURNAL Submitted (13-MAR-2002) Haenze J., Internal Medicine II / Biochemistry, University of Giessen, Friedrichstr. 24, 35392, GERMANY

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QY	1407 GTTGAGCAGGAATTTGGGGTCAACCCCTTTGCTTCTATCTTGAATFCCAATCTGGTACAA 1466
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RESULT 10

AF539799

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AF539799 1692 bp mRNA linear ROD 03-FEB-2003
Mus musculus NADPH oxidase 1 alpha mRNA, complete cds.
AF539799.1 GI:25573159
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 1692)
Banfi,B., Clark,R.A., Steger,K. and Krause,K.-H.
Two Novel Proteins Activate Superoxide Generation by the NADPH
Oxidase NOX1
J. Biol. Chem. 278 (6), 3510-3513 (2003)
12473664
2 (bases 1 to 1692)

AUTHORS Banfi, B. and Krause, K.-H.
 TITLE Direct Submission
 JOURNAL Submitted (21-AUG-2002) Dept. of Geriatrics, University Hospitals of Geneva, Chemin du Petit-Bel-Air 2, Geneva CH-1225, Switzerland

FEATURES
 Location/Qualifiers
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 387 AATTTTAAAGCAGCGTATCTGCTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 446
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Db 1790 CAATTCTACTTCAACAAAGAAACGTTCTGAATTGGAGGAGCCGACAGTAGT 1842

RESULT 12
AF152963
LOCUS
DEFINITION Rattus norvegicus NADH/NADPH mitochondrial subunit p65-mox
RNA, complete cds.
ACCESSION AF152963
VERSION AF152963.1 GI:5081797
KEYWORDS Rattus norvegicus (Norway rat)
SOURCE Rattus norvegicus
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 2577)
AUTHORS Suh, Y.A., Arnold, R.S., Lassee, B., Shi, J., Xu, X., Sorescu, D.,
Chung, A.B., Griendling, K.K. and Lambeth, J.D.
JOURNAL Nature 401 (6748), 79-82 (1999)
MEDLINE 99413719
PUBMED 10485709
REFERENCE 2 (bases 1 to 2577)
AUTHORS Lassee, B.
JOURNAL Direct Submission
TITLE Submitted (19-MAY-1999) Cardiology, Emory University, 1639 Pierce
Drive, 319 WMB, Atlanta, GA 30322, USA
JOURNAL
FEATURES
source
Location/Qualifiers
1. .2577
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Matches 1495; Conservative 0; Mismatches 295; Indels 3; Gaps 1;

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DB 173 GTTTCCTGTTGGGCTGAACATTTTCTGTTGTGATGATCCCTTCCTGAAATATGAGA 232
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ORIGIN
Query Match 50.08; Score 1305; DB 10; Length 2577;
Best Local Similarity 83.4%; Pred. No. 1.3e-289;
Matches 1495; Conservative 0; Mismatches 295; Indels 3; Gaps 1;

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RESULT 14

AY174116
LOCUS 1353 bp mRNA linear ROD 15-JAN-2003
DEFINITION Mus musculus NOX1 (Nox1) mRNA, partial cds.
ACCESSION AY174116
VERSION AY174116.1 GI:27762622

KEYWORDS

Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 1353)
Matsumoto, Y. and Blanchard, T. G.
Nox1 expression in the gastric mucosa of Helicobacter-infected

AUTHORS

gp1phox/- mice

TITLE

Unpublished

JOURNAL

2 (bases 1 to 1353)

AUTHORS

Matsumoto, Y. and Blanchard, T. G.

TITLE

Direct Submission

JOURNAL

Submitted (06-NOV-2002) Pediatrics, Case Western Reserve

UNIVERSITY

University, 2101 Adelbert Road, Cleveland, OH 44106, USA

FEATURES

Location/Qualifiers

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ORIGIN

Query Match 39.7%; Score 1036.6; DB 10; Length 1353;

Best Local Similarity 85.8%; Pred. No. 8.3e-228;

Matches 1163; Conservative 0; Mismatches 189; Indels 3; Gaps 1;

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QY 527 GATCTGCCTACATACAGCTATTTCATCATATTCGACACCTGTTTAACTTTGACTGCTATAG 586

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Db 62 GATCTGCATATTCACAGTTATTATCATATCATTTGACACCTATTAACTTCGAACGCTACAG 121
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QY 1787 AGTTTCTTATGTCGCTCGACTTTGGCAAGA 1821

Db 1319 GGTTCCTTATGTCGCTCGACTTTGGCAAAA 1353

RESULT 15

HS146H21/c

LOCUS

DEFINITION

Human DNA sequence from clone RPl-146H21 on chromosome Xq22

Contains cleavage stimulation factor, 64 KD subunit, gene similar to CYTOCHROME B-245 HEAVY CHAIN. pseudogene similar to hmrNP A1 protein and ESTs, complete sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 66424)

Lloyd, D.

Direct Submission

Submitted (05-JUN-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Dec 8, 1998 this sequence version replaced gi:3559852.

----- Genome Center

Center: Wellcome Trust Sanger Institute

Center code: SC

Web site: <http://www.sanger.ac.uk>

Contact: humquerry@sanger.ac.uk

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: EMBL; Sw: SWISSPROT; Tr: TrEMBL; Wp: WORMPEP; Information on the WORMPEP database can be found at <http://www.sanger.ac.uk/projects/C-elegans/wormpep> This sequence was generated from part of bacterial clone contigs of human chromosome X, constructed by the Sanger Centre Chromosome X Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/ChrX>

RPl-146H21 is from the library RPl-1 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm>

VECTOR: pCVPAC2

IMPORTANT: This sequence is not the entire insert of clone RPl-146H21. It may be shorter because we sequence overlapping sections only once, except for a short overlap.

The true left end of clone RPl-146H21 is at 1 in this sequence. The

true left end of clone LLOXNC01-131B10 is at 66325 in this sequence. The true right end of clone RPl-347M6 is at 25559 in this sequence.

FEATURES

source

Location/Qualifiers

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/chromosome="X"

/map="q22"

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/clone_lib="RPl-1"

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677..4270

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/note="35 copies 2 mer tt 67% conserved"

complement(1589..1704)

/note="match: STS: Em:AA422081"

2304..2604

/note="AluDb repeat: matches 1..300 of consensus"

3294..3369

/note="L1MD3 repeat: matches 7662..7739 of consensus"

3640..3867

/note="MER20 repeat: matches 2..218 of consensus"

4068..4270

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7655..7759

/note="MIR repeat: matches 6..117 of consensus"

7760..8069

/note="AluSx repeat: matches 2..312 of consensus"

8070..8215

/note="MIR repeat: matches 117..240 of consensus"

8393..8949

/note="L1MB7 repeat: matches 5606..6165 of consensus"

8950..9131

/note="AluSg repeat: matches 141..302 of consensus"

9132..9423

/note="AluY repeat: matches 1..293 of consensus"

9424..9558

/note="AluSg repeat: matches 1..141 of consensus"

9559..9708

/note="L1MB7 repeat: matches 5458..5607 of consensus"

9960..9991

/note="16 copies 2 mer tc 93% conserved"

10034..10244

/note="MIR repeat: matches 70..261 of consensus"

10245..10543

/note="AluSx repeat: matches 1..299 of consensus"

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/note="MIR repeat: matches 13..70 of consensus"

10821..11123

/note="AluSg repeat: matches 1..302 of consensus"

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/note="match: GSS: Em:B81269"
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/pseudo
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repeat_region 23446..24012
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repeat_region 25014..25259
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repeat_region 26356..26413
/note="MIR repeat: matches 6..262 of consensus"
repeat_region 26364..26422
/note="L2 repeat: matches 199..252 of consensus"
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Query Match

24.2%; Score 630.6; DB 9; Length 66424;

Best Local Similarity 91.3%; Pred. No. 2.7e-134;
Matches 735; Conservative 0; Mismatches 8; Indels 62; Gaps 4;
Qy 1772 CAAGTCGTAGTGGAGCTTTCTTATGTGGCCCTCGGACITTTGGCAAGAGCCTGGCGAA 1831
Db 7419 CAGGTCGTAGTGGAGCTTTCTTATGTGGCCCTCGGACITTTGGCAAGAGCCTGGCGAA 7360
Qy 1832 ATGCTGTACCGCATATTCCAGTCTGGATCTAGAAAGTTCAATTTACTTCAACAAAGA 1891
Db 7359 ATGCTGTACCGCATATTCCAGTCTGGATCTAGAAAGTTCAATTTACTTCAACAAAGA 7300
Qy 1892 AAATTTTGTAGTATAGGAATAAGGACGGTAATCTGCATTTTGTCTTGTATCTTCAG 1951
Db 7299 AAATTT-----7294

Qy 1952 TAATTGAGTTATAGGAATAAGGACGGTAATCTGCATTTTGTCTTGTATCTTCAGTAA 2011
Db 7293 ---TTGAGTTATAGGAATAAGGACGGTAATCTGCATTTTGTCTTGTATCTTCAGTAA 7237
Qy 2012 TTTACTTTGGTCTCMTGAGGTTTGANCACTCCTTTAGGATAAGAAATGTGCTCTCAAGCC 2071
Db 7236 TTTACTTTGGTCTCGTCAGGTTTGGAGCAGTCACCTTAGGATAAGAAATGTGCTCTCAAGCC 7177
Qy 2072 TTGACTCCCTGGTATTCTTTTGTATTGATTCACTTCGTTACTTGGAGCTTCAGCAAC 2131
Db 7176 TTGACTCCCTGGTATTCTTTTGTATTGATTCACTTCGTTACTTGGAGCTTCAGCAAC 7117
Qy 2132 TTAAGAACTTCTGAAGTTCTTAAAGTTCTGAANTTCTTAAAGCCCATGGATCTTCTCA 2191
Db 7116 TTAAGAACTTCTGAAGTTCTTAAAGTTCTGAAGTTCTTAAAGCCCATGGATCTTCTCA 7057
Qy 2192 GAAATAACTGTAAATCTTTCTGGACAGCCATGACTGTAGCAAGGCTTGATAGCAGAAG 2251
Db 7056 GAAATAACTGTAAATCTTTCTGGACAGCCATGACTGTAGCAAGGCTTGATAGCAGAAG 6997
Qy 2252 TTTGGTGGTTCAANAATTATACAACTAATCCAGGTGATTTTATCAATTCCAGTGTACCA 2311
Db 6996 TTTGGTGGTTCAAGTTATACAACTAATCCAGGTGATTTTATCAATTCCAGTGTACCA 6937
Qy 2312 TCTCCTGAGTTTGGTTTGAATCTTTTGTCCCTCCACCCCCACAGAAAGTTT-TAAGT 2370
Db 6936 TCTCCTGAGTTTGGTTTGAATCTTTTGTCCCTCCACCCCCACAGAAAGTTTCTAAGT 6877
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Qy 2491 TTACTGTCACTTTTGATATGGT-TTATCCAGTGTGAACAGCAATTTA---TTATTTTTC 2546
Db 6756 TTACTGTCACTTTTGATATGGTCTTATCCAGTGTGAACAGCAATTTTATTTCTTTTTC 6697
Qy 2547 TCATCAAAAAATAAAGGATTTTTTT 2571
Db 6696 TCATCAAAAAATAAAGGATTTTCTT 6672

Search completed: July 23, 2004, 11:33:18
Job time : 9959 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 23, 2004, 05:01:18 ; Search time 1001 Seconds
(without alignments)
11072.476 Million cell updates/sec

Title: US-10-618-839-1
Perfect score: 2609
Sequence: 1 gctgatagcacagtcttctgtc.....aaaaaaaaaaaaaaaaaaaaa 2609

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq_29Jan04:.*
1: geneseqn1980s.*
2: geneseqn1990s.*
3: geneseqn2000s.*
4: geneseqn2001as.*
5: geneseqn2001bs.*
6: geneseqn2002s.*
7: geneseqn2003as.*
8: geneseqn2003bs.*
9: geneseqn2003cs.*
10: geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2605	99.8	2609	3	AAD00692 Human mit
2	2605	99.8	2609	6	Abk27805 Human col
3	2605	99.8	2609	7	Ada83892 Human NOX
4	2593	99.4	2608	6	Abk37993 Human col
5	1820.2	69.8	1881	6	Abk37991 Human col
6	1305	50.0	2577	3	AAD00694 Rat mitog
7	1182.8	45.3	2619	3	AAD00695 Rat mitog
8	630.6	24.2	7517	4	Aak89061 Human dig
9	587.6	22.5	1192	4	Aak87743 Human dig
10	582	22.3	4266	7	Acc00438 Human gp9
11	582	22.3	4324	6	Aas94941 Human DNA
12	579.4	22.2	4267	6	Abk84501 Human cdn
13	551.6	21.1	658	6	Abk37992 Human col
14	551.6	21.1	658	6	Ada83893 Human NOX
15	521.2	20.0	2044	3	AAD00693 Human mit
16	521.2	20.0	2044	7	AAL50289 Human nox
17	501.2	19.2	560	6	Abq58274 Human col
18	479.2	18.4	503	7	AAD5537 Human col
19	478.8	18.4	558	6	Abk36930 Human col
20	468.6	18.0	491	6	Abk27790 Human col
21	468.6	18.0	562	6	Abq58190 Human col
22	460.6	17.7	573	6	Abk38268 Human col
23	446.2	17.1	449	6	Abk38185 Human col

24	423.6	16.2	579	6	ABQ57805	Abq57805 Human col
25	418	16.0	586	6	ABQ58832	Abq58832 Human col
26	414.2	15.9	3435	5	AAS69253	Aas69253 DNA encod
27	409.4	15.7	3435	5	AAS68641	Aas68641 DNA encod
28	405.4	15.5	428	3	AZ45660	Aaz45660 DNA sequ
29	386.4	14.8	493	4	AAH35144	Aan35144 Human col
30	383	14.7	519	6	ABQ57452	Abq57452 Human col
31	371.6	14.2	509	6	ABQ57779	Abq57779 Human col
32	362.2	13.9	381	6	ABK27596	Abk27596 Human col
33	333.8	12.8	447	6	ABQ59120	Abq59120 Human col
34	331	12.7	331	4	AAS39045	Abq59045 Novel hum
35	326.8	12.5	339	4	AAS39162	Aas39162 Novel hum
36	322.4	12.4	464	6	ABQ59160	Abq59160 Human col
37	319.8	12.3	399	5	AAF64565	Aaf64565 Novel hum
38	303	11.6	894	6	ABK27798	Abk27798 Human col
39	298.8	11.5	316	6	ABK44925	Abk44925 CDNA enco
40	296.2	11.4	609	6	ABQ58062	Abq58062 Human col
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42	233.4	8.9	306	4	AAS38444	Aas38444 Novel hum
43	207.4	7.9	3999	7	AAL50288	Aal50288 Human nox
44	84.6	3.2	2766	6	ABZ12979	Abz12979 Arabidops
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ALIGNMENTS

RESULT 1	
AAD00692	
ID	AAD00692 standard; cDNA; 2609 BP.
XX	
AC	AAD00692;
XX	
DT	08-SEP-2000 (first entry)
XX	
DE	Human mitogenic regulator mox1 cDNA.
XX	
KW	Human; mitogenic regulator; mox1; mitogenic oxidase; p65mox; superoxide;
KW	reactive oxygen intermediate; ROI; cell division; cytosolic;
KW	antiproliferative; cardiant; antiarteriosclerotic; vasotrophic;
KW	antiangiogenic; hypotensive; drug development; treatment; cancer;
KW	abnormal growth; psoriasis; prostatic hypertrophy; proliferation;
KW	blood vessel; lymphatic vessel; benign prostatic hypertrophy;
KW	cardiovascular disease; arteriovenous malformation; eye disorder;
KW	hypertension; atherosclerosis; restenosis; angioplasty; ss.
XX	
OS	Homo sapiens.
XX	
FH	Key Location/Qualifiers
FT	CDS 207..1901
FT	/*tag= a
FT	/*product= "Mox1"
XX	/*note= "mitogenic oxidase"
XX	
PN	WO2000028031-A2.
XX	
PD	18-MAY-2000.
XX	
PF	10-NOV-1999; 99WO-US026592.
XX	
PR	10-NOV-1998; 98US-0107911P.
PR	17-AUG-1999; 99US-0149332P.
PR	27-AUG-1999; 99US-0151242P.
XX	
PA	(UYEM-) UNIV EMORY.
XX	
PI	Lambeth JD, Lassegue BP, Griending KK, Arnold RS, Guangjie C;
XX	
DR	WPI; 2000-376545/32.
DR	P-PSDB; AAY71119.
XX	
PT	Protein capable of stimulating superoxide production, useful for treating conditions associated with abnormal growth, including cancer.

Db 361 GTGCCCAGGCGTCTGCTCTCTGTTGAATTTTAAACAGCAGCGTGATCCTGCTTCCCTGTGT 420
 Qy 421 GTCCCAATCTGCTCTCTCTCTGAGGGGCACTCTCTCAATTTTGAGCGCGCACACTGAGAA 480
 Db 421 GTCCCAATCTGCTCTCTCTCTGAGGGGCACTCTCTCAATTTTGAGCGCGCACACTGAGAA 480
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 Db 601 CCACAGATGGCTCCCTTGGCTCCATTTCTCTCCAGCCTATCTCATGATGAGAGAAAGGGGG 660
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 Db 781 CTACTGAGTTTCATCCGGAGGAGTTATTTTGAAGTCTTCTGGTATACTCACACCTTTTAA 840
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 Db 841 TCTTCTATATCTTGGCTTAGGGATTCACGGCATTTGGTGGAAATTTCTCGGGGTCAACAG 900
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 Db 961 ATCGTGACTCCCATCTGTAGGCGCCCTAAAGTTTGAAGGGATCCCGCTGAGTCTTGGAAAGT 1020
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 Qy 1381 TTTTTCAGTATGAAGTGGCTGTCTGTTGGAGCAGGAATTTGGGTCACCCCTTTGCTT 1440
 Db 1381 TTTTTCAGTATGAAGTGGCTGTCTGTTGGAGCAGGAATTTGGGTCACCCCTTTGCTT 1440
 Qy 1441 CTATCTTGAATCCATCTGGTACAAATTCAGTGTGCAGACCAACCTCAAAACAAAAA 1500
 Db 1441 CTATCTTGAATCCATCTGGTACAAATTCAGTGTGCAGACCAACCTCAAAACAAAAA 1500

Qy 1501 AGATCTATTTCTACTGGATCTGAGGAGAGCAGGTGCTTTTCTCTGGTCTCAACCAACCTGT 1560
 Db 1501 AGATCTATTTCTACTGGATCTGAGGAGAGCAGGTGCTTTTCTCTGGTCTCAACCAACCTGT 1560
 Qy 1561 TGACTTCCCTGGAAACAGGAGATGGAGAAATAGGCAAGTGGGTTTCTAAACTACCGTC 1620
 Db 1561 TGACTTCCCTGGAAACAGGAGATGGAGAAATAGGCAAGTGGGTTTCTAAACTACCGTC 1620
 Qy 1621 TCTTCTCCTCAGCGGATGGGACAGCAATATTTGTGTGTCATGCGACATATAAACTTTGCAAGG 1680
 Db 1621 TCTTCTCCTCAGCGGATGGGACAGCAATATTTGTGTGTCATGCGACATATAAACTTTGCAAGG 1680
 Qy 1681 CCATGACATCTGACAGGTCTGAAACAGAAAACCTCTTTGGGAGACCAATGTGGGACA 1740
 Db 1681 CCATGACATCTGACAGGTCTGAAACAGAAAACCTCTTTGGGAGACCAATGTGGGACA 1740
 Qy 1741 ATGAGTTTCTTACAATAGTACTCTCCACCCCAAGTCTGTAGTGGGAGTCTTCTTATGTG 1800
 Db 1741 ATGAGTTTCTTACAATAGTACTCTCCACCCCAAGTCTGTAGTGGGAGTCTTCTTATGTG 1800
 Qy 1801 GCCCTCGGACTTTGGGCAAGAGCCTGGGCAAAATGCTGTCAACGATATTCAGTCTGGATC 1860
 Db 1801 GCCCTCGGACTTTGGGCAAGAGCCTGGGCAAAATGCTGTCAACGATATTCAGTCTGGATC 1860
 Qy 1861 CTAGAAAAGTTCAATTTCTACTTCAACAAAGAAAATTTTGGAGTTATAGGAATAGGACGG 1920
 Db 1861 CTAGAAAAGTTCAATTTCTACTTCAACAAAGAAAATTTTGGAGTTATAGGAATAGGACGG 1920
 Qy 1921 TAACTGCAATTTGCTCTTTTGTATCTTCACTAATTTAGTATATAGGAATAAGGACGGTAA 1980
 Db 1921 TAACTGCAATTTGCTCTTTTGTATCTTCACTAATTTAGTATATAGGAATAAGGACGGTAA 1980
 Qy 1981 TCTGCAATTTGCTCTTTTGTATCTTCACTAATTTAGTATATAGGATTTGANCAGT 2040
 Db 1981 TCTGCAATTTGCTCTTTTGTATCTTCACTAATTTAGTATATAGGATTTGANCAGT 2040
 Qy 2041 CACTTTAGGATAGAAATGCGCTCTCAAGCCTGCACTCCCTGGTATCTTTTGTGATG 2100
 Db 2041 CACTTTAGGATAGAAATGCGCTCTCAAGCCTGCACTCCCTGGTATCTTTTGTGATG 2100
 Qy 2101 CATTCAAATCTGTTTACTTGGAGCTTCAAGCACTTAAAGAACTTCTGAAGTCTTAAAGTCT 2160
 Db 2101 CATTCAAATCTGTTTACTTGGAGCTTCAAGCACTTAAAGAACTTCTGAAGTCTTAAAGTCT 2160
 Qy 2161 GAANTTTTAAAGCCATGGATCTTCTCAGAAAATAAATCTGTAAGTCTTCTGAGCAG 2220
 Db 2161 GAANTTTTAAAGCCATGGATCTTCTCAGAAAATAAATCTGTAAGTCTTCTGAGCAG 2220
 Qy 2221 CCATGACTGTAGCAAGGCTTGATAGCAGAAAGTTTGGTGGTTCANAAATTAACAATAATC 2280
 Db 2221 CCATGACTGTAGCAAGGCTTGATAGCAGAAAGTTTGGTGGTTCANAAATTAACAATAATC 2280
 Qy 2281 CCAGTGAATTTTATCAATTCAGTGTACCACTCTCCTGAGTCTTGGTGTGTAATCTTTTG 2340
 Db 2281 CCAGTGAATTTTATCAATTCAGTGTACCACTCTCCTGAGTCTTGGTGTGTAATCTTTTG 2340
 Qy 2341 TCCCTCCCAACCCCAAGAGATTTTAAAGTGGTGAATTTTAAATATAAATTTTATGGA 2400
 Db 2341 TCCCTCCCAACCCCAAGAGATTTTAAAGTGGTGAATTTTAAATATAAATTTTATGGA 2400
 Qy 2401 ATAAATTAATGATAAACAATATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 2460
 Db 2401 ATAAATTAATGATAAACAATATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 2460
 Qy 2461 ATCCCAATATAACACCAACAGTGTACATGTTTACTGTCACTTTTGTATGTTTATCCAG 2520
 Db 2461 ATCCCAATATAACACCAACAGTGTACATGTTTACTGTCACTTTTGTATGTTTATCCAG 2520
 Qy 2521 TGTGAGCAGCAATTTATTTTGTCTCATCAAAAAATAAAGATTTTTCACATTTGAA 2580
 Db 2521 TGTGAGCAGCAATTTATTTTGTCTCATCAAAAAATAAAGATTTTTCACATTTGAA 2580

QY 2581 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2609
 Db ||||||| 2581 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2609

RESULT 3
 ADA83892
 ID ADA83892 standard; DNA; 2609 BP.
 XX AC ADA83892;
 XX 20-NOV-2003 (first entry)
 XX Human NOX1 gene.
 XX human; marker; expressed sequence tag; EST; arabidopsis; tumour;
 KW stress-induced phenotype; hyperosmotic stress; colon cancer; immunogen;
 KW vaccine; ds; gene.
 XX OS Homo sapiens.
 XX PN WO2002103028-A2.
 XX 27-DEC-2002.
 XX 30-MAY-2002; 2002WO-IB004189.
 XX 30-MAY-2001; 2001US-0293999P.
 PR 22-OCT-2001; 2001US-0330457P.
 PR 19-FEB-2002; 2002US-0357144P.
 XX (BIOM-) BIOMEDICAL CENT.
 XX Baranova AV, Yankovsky NK, Kozlov AP, Lobashev AV, Krukovskaya LI;
 PI WPI; 2003-175241/17.
 DR P-PSDB; ADA83894.
 XX Determining if a nucleic acid is a marker for a phenotype/cell type of
 PT interest, by global comparison of expressed sequence tags known to be
 PT expressed in the phenotype/cell type with all ESTs expressed in normal
 PT tissue.
 XX Claim 23; Page 292-294; 516pp; English.

CC The invention relates to a novel method for determining if a nucleic acid
 CC is a marker for a predetermined phenotype/cell type of interest from a
 CC biological species. The method comprises performing a global comparison
 CC of a group of expressed sequence tags (ESTs) known to be expressed in the
 CC phenotype/cell type of interest with all ESTs expressed in normal tissue
 CC in order to identify ESTs that are preferentially expressed in the
 CC phenotype/cell type of interest. A method of the invention is useful for
 CC determining whether a nucleic acid is a marker for a predetermined
 CC phenotype or cell type of interest from a biological species, preferably
 CC Arabidopsis or human. The cell type of interest is an abnormal cell such
 CC as a tumour cell, and the predetermined phenotype is a stress-induced
 CC phenotype such as hyperosmotic stress or high salt conditions. A method
 CC of the invention is also useful for determining the progression of colon
 CC cancer in a human, for detecting a tumour cell, and for regulating or
 CC preventing the growth of a tumour cell. An antibody of the invention is
 CC useful for detecting the absence or presence of peptides encoded by
 CC tumour-associated markers. A polypeptide of the invention is useful as an
 CC immunogen for vaccinating an animal. The present sequence encodes a
 XX tumour-associated antigen of the invention.

XX Sequence 2609 BP; 703 A; 574 C; 549 G; 779 T; 0 U; 4 Other;
 Query Match 99.8%; Score 2605; DB 7; Length 2609;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2609; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGATAGCACAGTCTCTGTCAGAGAAGGAGCGGAATAAACTTATTCATTCCTCCAGGAA 60
 |||||||

Db 1 GCTGATAGCACAGTCTCTGTCAGAGAAGGAGCGGAATAAACTTATTCATTCCTCCAGGAA 60
 QY 61 CTCTTGGGGTAGGTGTGTGTTTTTTCATCTTAAAGGCTCACAGACCTCGGTGGACAA 120
 ||||||| 61 CTCTTGGGGTAGGTGTGTGTTTTTTCATCTTAAAGGCTCACAGACCTCGGTGGACAA 120
 ||||||| 121 ATGTTCCATTCTCTGAAGGACCTCTCCAGAAATCCGGATTGCTGAATCTTCCCTGTGCTTA 180
 ||||||| 121 ATGTTCCATTCTCTGAAGGACCTCTCCAGAAATCCGGATTGCTGAATCTTCCCTGTGCTTA 180
 ||||||| 181 GAAGGGCTCCAAACACCTCTTGACAATGGGAACTGGGTGGTTAACCACTGGTTCAG 240
 ||||||| 181 GAAGGGCTCCAAACACCTCTTGACAATGGGAACTGGGTGGTTAACCACTGGTTCAG 240
 ||||||| 241 TTTTGTCTCTGGTGTGTGTTAGGCTGAATCTTTCCTGTTTCTGTTTGGAGTCCCTCTGA 300
 ||||||| 241 TTTTGTCTCTGGTGTGTGTTAGGCTGAATCTTTCCTGTTTCTGTTTGGAGTCCCTCTGA 300
 ||||||| 301 AATATCAGAAAGCCGACAAATCTACTACAGAAAAAATCCCTGGGTCAACATTGGCCT 360
 ||||||| 301 AATATCAGAAAGCCGACAAATCTACTACAGAAAAAATCCCTGGGTCAACATTGGCCT 360
 ||||||| 361 GTGCCCGAGGCTCTCTCTGCTTGAATTTTAAAGACGCTGATCTCTGCTTCCTGTGT 420
 ||||||| 361 GTGCCCGAGGCTCTCTCTGCTTGAATTTTAAAGACGCTGATCTCTGCTTCCTGTGT 420
 ||||||| 421 GTGCAATCTGCTGTCTCTTCTGAGGGGCACTGCTCATTTTGCAGCCGACACTGAGAA 480
 ||||||| 421 GTGCAATCTGCTGTCTCTTCTGAGGGGCACTGCTCATTTTGCAGCCGACACTGAGAA 480
 ||||||| 481 AGCAATTGATCACAACCTCACCTTCCACAAGCTGGTGGCTATATGATCTGCCTACATA 540
 ||||||| 481 AGCAATTGATCACAACCTCACCTTCCACAAGCTGGTGGCTATATGATCTGCCTACATA 540
 ||||||| 541 CAGCTATTTCACATCTGACACCTGTTTAACTTTGACTGCTATAGCAGAACGCGACAGG 600
 ||||||| 541 CAGCTATTTCACATCTGACACCTGTTTAACTTTGACTGCTATAGCAGAACGCGACAGG 600
 ||||||| 601 CCACAGATGGCTCCCTTGGCTCCATCTCTCCAGGCTATCTCATGATGAGAAAAAGGGG 660
 ||||||| 601 CCACAGATGGCTCCCTTGGCTCCATCTCTCCAGGCTATCTCATGATGAGAAAAAGGGG 660
 ||||||| 661 GTTCTGGCTAAATCCCATCCAGTCCGAAACACAGACAGTGGAGTATGTGACATTACCA 720
 ||||||| 661 GTTCTGGCTAAATCCCATCCAGTCCGAAACACAGACAGTGGAGTATGTGACATTACCA 720
 ||||||| 721 GGTGCTGGTCTCACTGGAGTGATCATGACAATAGCCTTGATTTCTCATGGTAACTTCAG 780
 ||||||| 721 GGTGCTGGTCTCACTGGAGTGATCATGACAATAGCCTTGATTTCTCATGGTAACTTCAG 780
 ||||||| 781 CTACTGAGTTTCATCCGGAGGAGTATTTTGAAGTCTTCTGGTATCTCACCACCTTTTAA 840
 ||||||| 781 CTACTGAGTTTCATCCGGAGGAGTATTTTGAAGTCTTCTGGTATCTCACCACCTTTTAA 840
 ||||||| 841 TCTTCTATATCTTGGCTTAGGATTACCGGCAATGGTGGAAATGTCGGGGTCAACAG 900
 ||||||| 841 TCTTCTATATCTTGGCTTAGGATTACCGGCAATGGTGGAAATGTCGGGGTCAACAG 900
 ||||||| 901 AGGAGGACATGAATGAGACTCATCTCGCAAGTGTGCAGAGTCTTTGAGATGTGGGATG 960
 ||||||| 901 AGGAGGACATGAATGAGACTCATCTCGCAAGTGTGCAGAGTCTTTGAGATGTGGGATG 960
 ||||||| 961 ATCTGTGACTCCCACTGTAGGCGCCCTTAAGTTTGAAGGGCATCCCCCTGAGTCTTGAAGT 1020
 ||||||| 961 ATCTGTGACTCCCACTGTAGGCGCCCTTAAGTTTGAAGGGCATCCCCCTGAGTCTTGAAGT 1020
 ||||||| 1021 GGATCTTGACCGGTCAATCTTTATATCTGTGAAAGGATCTCCGGTTTTTACCGTCCC 1080
 ||||||| 1021 GGATCTTGACCGGTCAATCTTTATATCTGTGAAAGGATCTCCGGTTTTTACCGTCCC 1080
 ||||||| 1081 AGCAGAGGTTGTGATTACCAAGGTTGTATGCACCCATCCAAAGTTTTTGGAAATGTCAGA 1140
 ||||||| 1081 AGCAGAGGTTGTGATTACCAAGGTTGTATGCACCCATCCAAAGTTTTTGGAAATGTCAGA 1140
 |||||||

QY 1141 TGAACAAGCGTGGCTTCAGCATGGAAGTGGGGCAGTATATCTTTGTTAAATTGCCCTCAA 1200
Db 1141 TGAACAAGCGTGGCTTCAGCATGGAAGTGGGGCAGTATATCTTTGTTAAATTGCCCTCAA 1200
QY 1201 TCTCTCTCCCTGGAATGGCATCCTTTTACTTTTGACCTCTGCTCCAGAGGAAGATTCTTCT 1260
Db 1201 TCTCTCTCCCTGGAATGGCATCCTTTTACTTTTGACCTCTGCTCCAGAGGAAGATTCTTCT 1260
QY 1261 CCATTTCATATCCGAGCAGCGGACCTGGACAGAAAAATCTCATAGGGCTTTTCGAAACAC 1320
Db 1261 CCATTTCATATCCGAGCAGCGGACCTGGACAGAAAAATCTCATAGGGCTTTTCGAAACAC 1320
QY 1321 AATATTACCAATTCAGGATTCAGTGGATGCTGCTTTGGCAGCAGCAAGCAGTGGAGTG 1380
Db 1321 AATATTACCAATTCAGGATTCAGTGGATGCTGCTTTGGCAGCAGCAAGCAGTGGAGTG 1380
QY 1381 TTTTCCAGTATGAAGTGGCTCTGCTGGTTGGAGCAGGAATTTGGGGTCAACCCCTTTGCTT 1440
Db 1381 TTTTCCAGTATGAAGTGGCTCTGCTGGTTGGAGCAGGAATTTGGGGTCAACCCCTTTGCTT 1440
QY 1441 CTATCTTGAATTCATCTGGTACAAAATTCAGTGTGCAGACCAAACTTCAAAAACAAAA 1500
Db 1441 CTATCTTGAATTCATCTGGTACAAAATTCAGTGTGCAGACCAAACTTCAAAAACAAAA 1500
QY 1501 AGATCTATTTTCTACTGGATCTGCAGGGAGACAGTGCCTTTTCTGTTTCAACACCTGT 1560
Db 1501 AGATCTATTTTCTACTGGATCTGCAGGGAGACAGTGCCTTTTCTGTTTCAACACCTGT 1560
QY 1561 TGACTTCCCTCGAAGCAGAGATGGAGGAATTTAGGCAAGTGGGTTTTCTAAACTACCGTC 1620
Db 1561 TGACTTCCCTCGAAGCAGAGATGGAGGAATTTAGGCAAGTGGGTTTTCTAAACTACCGTC 1620
QY 1621 TCTTCTCACCGGATGGGACAGCAATATTTGTTGTCATGAGCAATTTAACTTTGACAAAG 1680
Db 1621 TCTTCTCACCGGATGGGACAGCAATATTTGTTGTCATGAGCAATTTAACTTTGACAAAG 1680
QY 1681 CCAGTGCATCTGCAGAGCTCTGAAACAGNAACCTCTTTGGGAGACCAATTTGGGACA 1740
Db 1681 CCAGTGCATCTGCAGAGCTCTGAAACAGNAACCTCTTTGGGAGACCAATTTGGGACA 1740
QY 1741 ATGAGTTTTTCTACATAGCTACCTCCCAAGCTCTGTAGTGGGAGTTTTCTTATGTG 1800
Db 1741 ATGAGTTTTTCTACATAGCTACCTCCCAAGCTCTGTAGTGGGAGTTTTCTTATGTG 1800
QY 1801 GCCCTCGACCTTTGCAAGAGCTGCGCAAAATGCTGTACCGATATTCAGTCTGGATC 1860
Db 1801 GCCCTCGACCTTTGCAAGAGCTGCGCAAAATGCTGTACCGATATTCAGTCTGGATC 1860
QY 1861 CTAGAAAGGTTCAATTTCTACTTCAACAAGAAAAATTTTGGAGTTATAGGAATAAGGACGG 1920
Db 1861 CTAGAAAGGTTCAATTTCTACTTCAACAAGAAAAATTTTGGAGTTATAGGAATAAGGACGG 1920
QY 1921 TAATTCGATTTTGTCTTTTGTATCTTTCAGTAAATGAGTTATAGGAATAAGGACGGTAA 1980
Db 1921 TAATTCGATTTTGTCTTTTGTATCTTTCAGTAAATGAGTTATAGGAATAAGGACGGTAA 1980
QY 1981 TCTGCAATTTTGTCTTTTGTATCTTTCAGTAAATTTACTTGGTCTCTGAGTTGANCAGT 2040
Db 1981 TCTGCAATTTTGTCTTTTGTATCTTTCAGTAAATTTACTTGGTCTCTGAGTTGANCAGT 2040
QY 2041 CACTTTAGGATAAGAAATGCTCTCAAGCCCTTGACTCCCTGGTATTTCTTTTTTGTG 2100
Db 2041 CACTTTAGGATAAGAAATGCTCTCAAGCCCTTGACTCCCTGGTATTTCTTTTTTGTG 2100
QY 2101 CATTCAACTTCGTTACTTTGAGCTTCAGCAACTTAAAGAACTTCTGAAAGTCTTAAAGTTCT 2160
Db 2101 CATTCAACTTCGTTACTTTGAGCTTCAGCAACTTAAAGAACTTCTGAAAGTCTTAAAGTTCT 2160
QY 2161 GAANTTCTTAAGCCCATGATCTTCTTCAGAAAAATAACGTAAATCTTCTGACAG 2220
Db 2161 GAANTTCTTAAGCCCATGATCTTCTTCAGAAAAATAACGTAAATCTTCTGACAG 2220

QY 2221 CCATGACTGTAGCAAGGCTTGATAGCAGAAAGTTTTGGTGGTTCAAAATTATACAACATAATC 2280
Db 2221 CCATGACTGTAGCAAGGCTTGATAGCAGAAAGTTTTGGTGGTTCAAAATTATACAACATAATC 2280
QY 2281 CCAGGTGATTTTATCAATTTCCAGTGTACCATTCTCCTGAGTTTTGGTGGTTTGAATCTTTTG 2340
Db 2281 CCAGGTGATTTTATCAATTTCCAGTGTACCATTCTCCTGAGTTTTGGTGGTTTGAATCTTTTG 2340
QY 2341 TCCCTCCACCCCCACAGAGATTTTAAAGTGGTGAATTTTAAATAAAAAATTTATTGA 2400
Db 2341 TCCCTCCACCCCCACAGAGATTTTAAAGTGGTGAATTTTAAATAAAAAATTTATTGA 2400
QY 2401 ATAATTATGATTAATAACATATAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 2460
Db 2401 ATAATTATGATTAATAACATATAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 2460
QY 2461 ATCCCATATATAACCAACAGTGTACATGTTTACTGTCTCTTTTGATATGTTTATCCAG 2520
Db 2461 ATCCCATATATAACCAACAGTGTACATGTTTACTGTCTCTTTTGATATGTTTATCCAG 2520
QY 2521 TGTGAACAGCAATTTTATTTTGTCTCATCAAAAAATAAAGGATTTTTTTCACCTTGAA 2580
Db 2521 TGTGAACAGCAATTTTATTTTGTCTCATCAAAAAATAAAGGATTTTTTTCACCTTGAA 2580
QY 2581 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2609
Db 2581 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2609

RESULT 4
ABK37993
ID ABK37993 standard; DNA; 2608 BP.
XX
AC ABK37993;
XX
DT 21-MAY-2002 (first entry)
XX
DE Human colon specific gene (CSG) Cln106.
XX
KW Human; colon specific; gene; CSG; gene; ds; cytostatic; metastasis;
KW colon cancer staging.
XX
OS Homo sapiens.
XX
PN WO200206515-A2.
XX
PD 24-JAN-2002.
XX
PF 17-JUL-2001; 2001WO-US022454.
XX
PR 17-JUL-2000; 2000US-(0618596.
XX
PA (DIAD-) DIADEXUS INC.
XX
PI Macina RA, Sun Y;
XX
DR WPI; 2002-171815/22.
XX
PT Diagnosing, staging or monitoring colon cancer involves determining a
PT colon specific gene in cells, tissues or body fluids in patient, and
PT comparing it with levels of the gene from a normal human control.
XX
PS Claim 7; Page 51-52; 52pp; English.
XX
CC The invention relates to diagnosing the presence of colon cancer,
CC metastases of colon cancer, staging colon cancer, monitoring colon cancer
CC for the onset of metastasis or monitoring a change in stage of colon
CC cancer in a patient. The method involves determining a colon specific
CC gene (CSG) in cells, tissues or bodily fluids and comparing it with
CC levels of CSG in cells, tissues or bodily fluids from a normal human
CC control. Colon cancer can be treated by administering a molecule which
CC down regulates the expression or activity of CSG. An immune response
CC against a target cell expressing CSG can be induced by delivering an

CC immunologically stimulatory amount of a CSG protein to a patient, so that
 CC an immune response is mounted. Therapeutic agents are useful for imaging
 CC colon cancer in a patient by administering an agent labelled with
 CC paramagnetic ions or a radioisotope to the patient. They are also useful
 CC for preventing the onset of colon cancer, and in diagnosis and treatment
 CC of the disease. This sequence represents a colon specific gene of the
 CC invention
 XX
 SQ Sequence 2608 BP; 703 A; 574 C; 548 G; 779 T; 0 U; 4 Other;

Query Match 99.4%; Score 2593; DB 6; Length 2608;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2608; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY	1	GCTGATAGCAGTTCGTCCAGAGAGGAGCGGAATAAATTAATCAATCCAGGAA	60
DB	1	GCTGATAGCAGTTCGTCCAGAGAGGAGCGGAATAAATTAATCAATCCAGGAA	60
QY	61	CTCTTGGGGTAGGTGTGTTTTCACATCTTAAGGCTCACAGACCTCGCTGGACAA	120
DB	61	CTCTTGGGGTAGGTGTGTTTTCACATCTTAAGGCTCACAGACCTCGCTGGACAA	120
QY	121	ATGTTCCATTCCTGAAGGAGCTCTCCAGAAATCCGGATTGCTGAATCTTCCCTGTGGCTA	180
DB	121	ATGTTCCATTCCTGAAGGAGCTCTCCAGAAATCCGGATTGCTGAATCTTCCCTGTGGCTA	180
QY	181	GAAGGGCTCCAAACCACTCTTGACAAATGGGAACTGGGTGGTTAAACCACTGGTTTTAG	240
DB	181	GAAGGGCTCCAAACCACTCTTGACAAATGGGAACTGGGTGGTTAAACCACTGGTTTTAG	240
QY	241	TTTTTGTCTGGTGTGTTGGTAGGCTGAATGTTTCTTCTGTTGGATGCTTCCTGA	300
DB	241	TTTTTGTCTGGTGTGTTGGTAGGCTGAATGTTTCTTCTGTTGGATGCTTCCTGA	300
QY	301	AATATGAGAGGCGCAATACTACTACAAAGAAATCCCTTGGTCAACATGGCCCT	360
DB	301	AATATGAGAGGCGCAATACTACTACAAAGAAATCCCTTGGTCAACATGGCCCT	360
QY	361	GTCCCGAGGCTGCTCTCTGTTGAAATTTTAAACAGACGCTGATCTCTGCTTCTGTGT	420
DB	361	GTCCCGAGGCTGCTCTCTGTTGAAATTTTAAACAGACGCTGATCTCTGCTTCTGTGT	420
QY	421	GTCCCAATCTGCTGCTCTCTGAGGGGCACTGCTCAATTTGCGCGGACACCTGAGAA	480
DB	421	GTCCCAATCTGCTGCTCTCTGAGGGGCACTGCTCAATTTGCGCGGACACCTGAGAA	480
QY	481	AGCAATTTGGATCACAACCTCACCTTCCCAAGCTGGTGGCTATATGATCTGCTACATA	540
DB	481	AGCAATTTGGATCACAACCTCACCTTCCCAAGCTGGTGGCTATATGATCTGCTACATA	540
QY	541	CAGCTATTACATCATTTGACACCTGTTTAACTTTGACTGCTATAGCAGAGCCGACAG	600
DB	541	CAGCTATTACATCATTTGACACCTGTTTAACTTTGACTGCTATAGCAGAGCCGACAG	600
QY	601	CCACAGATGGCTCCCTTGTCTCAATCTCTCCAGCCTATCTCATGATGAGAAAGGGG	660
DB	601	CCACAGATGGCTCCCTTGTCTCAATCTCTCCAGCCTATCTCATGATGAGAAAGGGG	660
QY	661	GTTCTTGGCTAAATCCATCCAGTCCGAAACACGACAGTGGAGTATGTGACATTCACCA	720
DB	661	GTTCTTGGCTAAATCCATCCAGTCCGAAACACGACAGTGGAGTATGTGACATTCACCA	720
QY	721	GGTTGCTGCTCACTGAGTGAATCATGACAAATAGCCTTGATTCATGTTAACTTCAG	780
DB	721	GGTTGCTGCTCACTGAGTGAATCATGACAAATAGCCTTGATTCATGTTAACTTCAG	780
QY	781	CTACTCAGTTTCATCCGGAGGATTTTGAAGTCTTCTGGTATCTACACCTTTTAA	840
DB	781	CTACTCAGTTTCATCCGGAGGATTTTGAAGTCTTCTGGTATCTACACCTTTTAA	840
QY	841	TCTTCTATATCTTGGCTTAGGAAATTCACGGCAATGGTGAATTTGCCGGGTCAAACAG	900
DB	841	TCTTCTATATCTTGGCTTAGGAAATTCACGGCAATGGTGAATTTGCCGGGTCAAACAG	900

QY	901	AGGAGAGCATGAATGAGAGTCACTCGCAAGTGTGCAGAGTCTTTTGAATGGGATG	960
DB	901	AGGAGAGCATGAATGAGAGTCACTCGCAAGTGTGCAGAGTCTTTTGAATGGGATG	960
QY	961	ATCGTGACTCCCACTGTAGGCGCCCTAAGTTTGAAGGGCATCCCTGAGTCTTGAAGT	1020
DB	961	ATCGTGACTCCCACTGTAGGCGCCCTAAGTTTGAAGGGCATCCCTGAGTCTTGAAGT	1020
QY	1021	GGATCCTTGCAACCGGTCATCTTTATATCTGTGAAGAGTCCCTCCGCTTTTACCGTCCC	1080
DB	1021	GGATCCTTGCAACCGGTCATCTTTATATCTGTGAAGAGTCCCTCCGCTTTTACCGTCCC	1080
QY	1081	AGCAGAAGGTTGTGATTTACCAAGTTGTTATGCAACCATCCAAAGTTTTCGAATTGCGA	1140
DB	1081	AGCAGAAGGTTGTGATTTACCAAGTTGTTATGCAACCATCCAAAGTTTTCGAATTGCGA	1140
QY	1141	TGAACAAGCGTGGCTTCAGCATGGAAGTGGGGCAGTATATCTTTGTTAAATGGCCCTCAA	1200
DB	1141	TGAACAAGCGTGGCTTCAGCATGGAAGTGGGGCAGTATATCTTTGTTAAATGGCCCTCAA	1200
QY	1201	TCTCTCTCTCGGAAATGSCATCTTTTACTTTTGACCTCTGCTCCAGAGGAAGATTTCTCT	1260
DB	1201	TCTCTCTCTCGGAAATGSCATCTTTTACTTTTGACCTCTGCTCCAGAGGAAGATTTCTCT	1260
QY	1261	CCATTTCATATCCGAGCAGCAGGGAATCTGACAGAAAATCTCAATAAGGGCTTTTGAACAAC	1320
DB	1261	CCATTTCATATCCGAGCAGCAGGGAATCTGACAGAAAATCTCAATAAGGGCTTTTGAACAAC	1320
QY	1321	AATATTTCACCAATTTCCAGGATTTGAAGTGGATGGTCCCTTTGGCACAGCAGTGGAGATG	1380
DB	1321	AATATTTCACCAATTTCCAGGATTTGAAGTGGATGGTCCCTTTGGCACAGCAGTGGAGATG	1380
QY	1381	TTTTCCAGTATGAAAGTGGCTGCTGTTTGGAGCAGGAATTTGGGGTCAACCCCTTTGCTT	1440
DB	1381	TTTTCCAGTATGAAAGTGGCTGCTGTTTGGAGCAGGAATTTGGGGTCAACCCCTTTGCTT	1440
QY	1441	CTATCTTGAATTCATCTGTTCAAAATCCAGTGTGCAGACCAACCAACCTCAAAACAATAA	1500
DB	1441	CTATCTTGAATTCATCTGTTCAAAATCCAGTGTGCAGACCAACCAACCTCAAAACAATAA	1500
QY	1501	AGATCTATTCTTCTGAGTCTGAGGAGACAGTGGCTTTCTCTGTTTCAACAACCTGT	1560
DB	1501	AGATCTATTCTTCTGAGTCTGAGGAGACAGTGGCTTTCTCTGTTTCAACAACCTGT	1560
QY	1561	TGACTTCTCCGAAACAGGAGATGGAGGAATTTAGGCAAGTGGTCTTCTAAACTACGGTC	1620
DB	1561	TGACTTCTCCGAAACAGGAGATGGAGGAATTTAGGCAAGTGGTCTTCTAAACTACGGTC	1620
QY	1621	TCTTCTCACCAGTGGGACAGCAATATTGTTGGTCTATGCGCATTTAAACTTTGACAAGG	1680
DB	1621	TCTTCTCACCAGTGGGACAGCAATATTGTTGGTCTATGCGCATTTAAACTTTGACAAGG	1680
QY	1681	CCACTGACATCTGTGACAGTCTGAAACAGAAACCTCTTTGGAGACCAATGTTGGACA	1740
DB	1681	CCACTGACATCTGTGACAGTCTGAAACAGAAACCTCTTTGGAGACCAATGTTGGACA	1740
QY	1741	ATGAGTTTTCTACAATAGTCTCTCCACCCCAAGTCTGTAGTGGAGTCTTCTTATGTG	1800
DB	1741	ATGAGTTTTCTACAATAGTCTCTCCACCCCAAGTCTGTAGTGGAGTCTTCTTATGTG	1800
QY	1801	GCCCTCGGACTTTGGCAAGAGCTTGGCAAAATGCTGTCAACGATATCCAGTCTCGATC	1860
DB	1801	GCCCTCGGACTTTGGCAAGAGCTTGGCAAAATGCTGTCAACGATATCCAGTCTCGATC	1860
QY	1861	CTAGAAAGGTTCAATCTCTCAACAAAGAAAATTTTTCAGTTATAGGAATAAGGACGG	1920
DB	1861	CTAGAAAGGTTCAATCTCTCAACAAAGAAAATTTTTCAGTTATAGGAATAAGGACGG	1920
QY	1921	TAATCTGCAATTTGCTCTTTGATCTTTCAGTAATTTAGTATAGGAATAAGGACGGTAA	1980
DB	1921	TAATCTGCAATTTGCTCTTTGATCTTTCAGTAATTTAGTATAGGAATAAGGACGGTAA	1980

QY 1981 TCTGCAATTTGTCCTCTGTTATCTTCAGTAATTTACTTGGTCTCCTCAGGTTTTCAGCAGT 2040
 Db |||||||
 QY 1981 TCTGCAATTTGTCCTCTGTTATCTTCAGTAATTTACTTGGTCTCCTCAGGTTTTCAGCAGT 2040
 Db |||||||
 QY 2041 CACTTTAGGATAAGAAATGCTCTCAAGCCCTTGACTCCCTGGTATCTTTTGTGATTG 2100
 Db |||||||
 QY 2041 CACTTTA-GATAAGAAATGCTCTCAAGCCCTTGACTCCCTGGTATCTTTTGTGATTG 2099
 Db |||||||
 QY 2101 CATTCAACTTCGTTACTTGAGCTTCAGCAACTTAAGAACTTCTGAAAGTTCTTAAGTTCT 2160
 Db |||||||
 QY 2100 CATTCAACTTCGTTACTTGAGCTTCAGCAACTTAAGAACTTCTGAAAGTTCTTAAGTTCT 2159
 Db |||||||
 QY 2161 GAANTTCTTAAAGCCCACTGATCTCTTCTCAGAAAATAAATCTGTAATCTTTCTGGACAG 2220
 Db |||||||
 QY 2160 GAANTTCTTAAAGCCCACTGATCTCTTCTCAGAAAATAAATCTGTAATCTTTCTGGACAG 2219
 Db |||||||
 QY 2221 CCATGACTGTAGCAAGGCTTGATAGCAGAAAGTTTGGTGGTTTCAANAATTAACAATATC 2280
 Db |||||||
 QY 2220 CCATGACTGTAGCAAGGCTTGATAGCAGAAAGTTTGGTGGTTTCAANAATTAACAATATC 2279
 Db |||||||
 QY 2281 CCAGTGATTTTATCAATTCAGTGTACCATCTCTGAGTTTGGTGGTTTCAATCTTTG 2340
 Db |||||||
 QY 2280 CCAGTGATTTTATCAATTCAGTGTACCATCTCTGAGTTTGGTGGTTTCAATCTTTG 2339
 Db |||||||
 QY 2341 TCCCTCCACCCACACAGAGATTTTAAAGTGGTGGTCTTTTAAATAAATAATTTATTGA 2400
 Db |||||||
 QY 2340 TCCCTCCACCCACACAGAGATTTTAAAGTGGTGGTCTTTTAAATAAATAATTTATTGA 2399
 Db |||||||
 QY 2401 ATAATTAATGATAAACAATAATAATAAATAAATAAATAAATAAATAAATAAATAAATAA 2460
 Db |||||||
 QY 2400 ATAATTAATGATAAACAATAATAATAAATAAATAAATAAATAAATAAATAAATAAATAA 2459
 Db |||||||
 QY 2461 ATCCCATATACACCAACAGTGTACATGTTTACTGTGTCATCTTTTGTATGTTTATCCAG 2520
 Db |||||||
 QY 2460 ATCCCATATACACCAACAGTGTACATGTTTACTGTGTCATCTTTTGTATGTTTATCCAG 2519
 Db |||||||
 QY 2521 TGTGAACAGCAATTTATTATTTTCTCATCAAAAATAAAGGATTTTTCATCTGAA 2580
 Db |||||||
 QY 2520 TGTGAACAGCAATTTATTATTTTGTCTCATCAAAAATAAAGGATTTTTCATCTGAA 2579
 Db |||||||
 QY 2581 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2609
 Db AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2608

RESULT 5
 ABK37991
 ID ABK37991 standard; DNA; 1881 BP.
 AC ABK37991;
 XX
 XX 21-MAY-2002 (first entry)
 DT Human colon specific gene (CSG) splice variant #1.
 DE Human; colon specific gene; CSG; gene; ds; cytostatic; metastasis;
 KW Human colon cancer staging.
 KW
 XX Homo sapiens.
 OS
 XX WO200206515-A2.
 PN
 XX 24-JAN-2002.
 PD
 XX 17-JUL-2001; 2001WO-US022454.
 PF
 XX 17-JUL-2000; 2000US-00618596.
 PR
 XX (DIAD-) DIADEXUS INC.
 PA
 XX Macina RA, Sun Y;
 PI
 XX WPI; 2002-171815/22.
 DR

DR P-PSDB; AAU85422.
 XX
 PT Diagnosing, staging or monitoring colon cancer involves determining a
 PT colon specific gene in cells, tissues or body fluids in patient, and
 PT comparing it with levels of the gene from a normal human control.
 XX
 PS Claim 7; Page 30-31; 52pp; English.
 XX
 CC The invention relates to diagnosing the presence of colon cancer,
 CC metastases of colon cancer, staging colon cancer, monitoring colon cancer
 CC for the onset of metastasis or monitoring a change in stage of colon
 CC cancer in a patient. The method involves determining a colon specific
 CC gene (CSG) in cells, tissues or bodily fluids and comparing it with
 CC levels of CSG in cells, tissues or bodily fluids from a normal human
 CC control. Colon cancer can be treated by administering a molecule which
 CC down regulates the expression or activity of CSG. An immune response
 CC against a target cell expressing CSG can be induced by delivering an
 CC immunologically stimulatory amount of a CSG protein to a patient, so that
 CC an immune response is mounted. Therapeutic agents are useful for imaging
 CC colon cancer in a patient by administering an agent labelled with
 CC paramagnetic ions or a radioisotope to the patient. They are also useful
 CC for preventing the onset of colon cancer, and in diagnosis and treatment
 CC of the disease. This sequence represents a colon specific gene of the
 CC invention
 XX
 SQ Sequence 1881 BP; 461 A; 443 C; 434 G; 543 T; 0 U; 0 Other;
 Query Match 69.8%; Score 1820.2; DB 6; Length 1881;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1822; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 137 GGACCTCTCCAGATCCGATTGCTGAATCTTCCCTGTGTGCTAGAGGGCTCCAAACCA 196
 Db |||||||
 QY 197 CCTCTTGACAAATGGGAAATCGGGTGGTTAAACCACTGGTTCAGTTTTCGTGTTGT 256
 Db |||||||
 QY 257 TTGGTAGGCTGAATGTTTCCCTGTGTGGATGCTTCTCTGAATATGAGAGCCGA 316
 Db |||||||
 QY 121 TTGGTAGGCTGAATGTTTCCCTGTGTGGATGCTTCTCTGAATATGAGAGCCGA 180
 Db |||||||
 QY 317 CAATACTACTACACAGAAAAATCCTTGGGTCAACATTTGGCTGTGCCGAGGCTCTGC 376
 Db |||||||
 QY 181 CAATACTACTACACAGAAAAATCCTTGGGTCAACATTTGGCTGTGCCGAGGCTCTGC 240
 Db |||||||
 QY 377 TCTCTGTTGMAATTTAAACAGCAGCTGATCCTGCTTCTGTGTGCGAATTCGTCTGC 436
 Db |||||||
 QY 241 TCTCTGTTGMAATTTAAACAGCAGCTGATCCTGCTTCTGTGTGCGAATTCGTCTGC 300
 Db |||||||
 QY 437 CTTCCTGAGGGGACCTGCTCATTTTGCAGCGCACCTGAGAAAGCAATTTGGATCAAA 496
 Db |||||||
 QY 301 CTTCCTGAGGGGACCTGCTCATTTTGCAGCGCACCTGAGAAAGCAATTTGGATCAAA 360
 Db |||||||
 QY 497 CCTCACCCTTCCACAAGCTGGTGGCTATATGATCTGCTTACATACAGTATTCATCAT 556
 Db |||||||
 QY 361 CCTCACCCTTCCACAAGCTGGTGGCTATATGATCTGCTTACATACAGTATTCATCAT 420
 Db |||||||
 QY 557 TGCACACCTGTTTAACTTTTGA CTGCTATAGCAGAACCGCAGGCGCAGATGGCTCCCT 616
 Db |||||||
 QY 421 TGCACACCTGTTTAACTTTTGA CTGCTATAGCAGAACCGCAGGCGCAGATGGCTCCCT 480
 Db |||||||
 QY 617 TGCCTCCATCTCTCCAGCCTATCTCATGATGAGAAAAAGGGGGTCTTGGCTAAATCC 676
 Db |||||||
 QY 481 TGCCTCCATCTCTCCAGCCTATCTCATGATGAGAAAAAGGGGGTCTTGGCTAAATCC 540
 Db |||||||
 QY 677 CATCCAGTCCCGAAACACAGCAGTGGAGTATGTGACATTCACACAGGTTTGGTGTCTAC 736
 Db |||||||
 QY 541 CATCCAGTCCCGAAACACAGCAGTGGAGTATGTGACATTCACACAGGTTTGGTGTCTAC 600
 Db |||||||
 QY 737 TGGAGTGATCAATGACAAATAGCCTTGATTCATGTTGTAATCTAGTCTACTGATTCATCG 796
 Db |||||||

Db 601 TGGAGTGATCATGACAAATGACCTTGATCTCATGGTAATCTCAGCTACTGAGTTCATCCG 660
QY 797 GAGGAGTTATTTGAAAGTCTTCTGGTATATCTCAACCTTTTATCTTCTATATCTCTTGG 856
Db 661 GAGGAGTTATTTGAAAGTCTTCTGGTATATCTCAACCTTTTATCTTCTATATCTCTTGG 720
QY 857 CTTAGGGATTCAGGGCATTTGGTGAATGTCGCGGGTCAACACAGAGAGAGCATGAATGA 916
Db 721 CTTAGGGATTCAGGGCATTTGGTGAATGTCGCGGGTCAACACAGAGAGAGCATGAATGA 780
QY 917 GAGTCATCTTCGCAAGTGTGACAGTCTTTTGAGATGTGGATGATCGTGACTCCCACTG 976
Db 781 GAGTCATCTTCGCAAGTGTGACAGTCTTTTGAGATGTGGATGATCGTGACTCCCACTG 840
QY 977 TAGCGGCCCTAAGTTTGAAGGCAATCCCTCTGAGTCTTGGAAAGTGATCTTGCACCGGT 1036
Db 841 TAGCGGCCCTAAGTTTGAAGGCAATCCCTCTGAGTCTTGGAAAGTGATCTTGCACCGGT 900
QY 1037 CATTCCTTTATATCTGTGAAGGATCTCCCGGTTTACCGCTCCACAGAGAGTGTGAT 1096
Db 901 CATTCCTTTATATCTGTGAAGGATCTCCCGGTTTACCGCTCCACAGAGAGTGTGAT 960
QY 1097 TACCAAGGTTGTTATGACCCATCCAAAGTTTGGAAATTCAGATGAACAAGCGTGCTT 1156
Db 961 TACCAAGGTTGTTATGACCCATCCAAAGTTTGGAAATTCAGATGAACAAGCGTGCTT 1020
QY 1157 CAGCATGGAAGTGGGAGTATATCTTTGTTAAATGCGCCCTCAATCTCTCTCGTGAATG 1216
Db 1021 CAGCATGGAAGTGGGAGTATATCTTTGTTAAATGCGCCCTCAATCTCTCTCGTGAATG 1080
QY 1217 GCATCCTTTTACTCTTGACCTCTGCTCCAGAGGAATTTCTTCCATCATATCCGAGC 1276
Db 1081 GCATCCTTTTACTCTTGACCTCTGCTCCAGAGGAATTTCTTCCATCATATCCGAGC 1140
QY 1277 AGCAGGGGACTGACAGAAATCTCATAAGGGCTTTCGAACAACAATATTCACCAATTC 1336
Db 1141 AGCAGGGGACTGACAGAAATCTCATAAGGGCTTTCGAACAACAATATTCACCAATTC 1200
QY 1337 CAGGATGGAAGTGGTCCCTTTGGCAGACGAGTGGATGTTTTCCAGTATGAAGT 1396
Db 1201 CAGGATGGAAGTGGTCCCTTTGGCAGACGAGTGGATGTTTTCCAGTATGAAGT 1260
QY 1397 GGCCTGCTGGTTGGAGCAGGAATGGGGTCAACCCCTTCTCTATCTTGAATCCAT 1456
Db 1261 GGCCTGCTGGTTGGAGCAGGAATGGGGTCAACCCCTTCTCTATCTTGAATCCAT 1320
QY 1457 CTGGTACAAATTCAGTGTGCAGACCAACCTCAAAACAAAAGATCTATTTCTACTG 1516
Db 1321 CTGGTACAAATTCAGTGTGCAGACCAACCTCAAAACAAAAGATCTATTTCTACTG 1380
QY 1517 GATCTCAGGGAGACAGTGGCTTTCTGGTTCAACACCTGTTGACTTCCCTGGAACA 1576
Db 1381 GATCTCAGGGAGACAGTGGCTTTCTGGTTCAACACCTGTTGACTTCCCTGGAACA 1440
QY 1577 GGAGATGGAGGAATTAGGCAAGTGGTTTCTAAACTACCGTCTCTCTCTACCGGATG 1636
Db 1441 GGAGATGGAGGAATTAGGCAAGTGGTTTCTAAACTACCGTCTCTCTCTACCGGATG 1500
QY 1637 GGACAGCAATATTGTTGGTCAATGAGCATTAATACTTTGACAGGCCACTGACATCGTGAC 1696
Db 1501 GGACAGCAATATTGTTGGTCAATGAGCATTAATACTTTGACAGGCCACTGACATCGTGAC 1560
QY 1697 AGTCTGAAACAGAAACCTCTTTGGGAGACCAATGTGGGCAATGAGTTCATCAAT 1756
Db 1561 AGTCTGAAACAGAAACCTCTTTGGGAGACCAATGTGGGCAATGAGTTCATCAAT 1620
QY 1757 AGTCTCTCCACCCCAAGTCTCTAGTGGAGTTCCTTATGTGGCCCTCGGACTTGGC 1816
Db 1621 AGTCTCTCCACCCCAAGTCTCTAGTGGAGTTCCTTATGTGGCCCTCGGACTTGGC 1680
QY 1817 AAAGAGCCTGCGCAATGTCTGTCACCGATATTCAGTCTGGATCTGTAGAAAGTTCAT 1876
Db 1681 AAAGAGCCTGCGCAATGTCTGTCACCGATATTCAGTCTGGATCTGTAGAAAGTTCAT 1740

QY 1877 CTACTTCAACAAAGAAAAATTTTGGTATAGGAATAAGCAGGTAATCTGCATTTTGTG 1936
Db 1741 CTACTTCAACAAAGAAAAATTTTGGTATAGGAATAAGCAGGTAATCTGCATTTTGTG 1800
QY 1937 TCTTTGTATCTTCAGTAATTGAGTT 1961
Db 1801 TCTTTGTATCTTCAGTAATTTACTT 1825

RESULT 6
AAD00694

ID AAD00694 standard; cDNA; 2577 BP.

XX AAD00694;

XX AC AC

XX 08-SEP-2000 (first entry)

XX Rat mitogenic regulator mox1 cDNA.

XX Rat; mitogenic regulator; mox1; mitogenic oxidase; p65mox; superoxide;
KW reactive oxygen intermediate; ROI; cell division; cytostatic;
KW antipsoriatic; cardiant; antiarteriosclerotic; vasotropic;
KW antiangiogenic; hypotensive; drug development; treatment; cancer;
KW abnormal growth; psoriasis; prostatic hypertrophy; proliferation;
KW blood vessel; lymphatic vessel; benign prostatic hypertrophy;
KW cardiovascular disease; arteriovenous malformation; eye disorder;
KW hypertension; atherosclerosis; restenosis; angioplasty; ss.

OS Rattus sp.

XX Key Location/Qualifiers
FH 5'UTR 1. .127
FT /*tag= a
FT CDS 128. 1819
FT /*tag= b
FT /*product= "Mox1"
FT /*note= "Mitogenic oxidase"
FT 3'UTR 1820. .2577
FT /*tag= c
FT polyA_signal 2201. .2206
FT /*tag= d
FT polyA_signal 2550. .2555
FT /*tag= e

PN W0200028031-A2.

PD 18-MAY-2000.

XX 10-NOV-1999; 99WO-US026592.

XX 10-NOV-1998; 98US-0107911P.

PR 17-AUG-1999; 99US-0149332P.

PR 27-AUG-1999; 99US-0151242P.

XX (UYEM-) UNIV EMORY.

XX Lambeth JD, Lassegue BP, Griendling KK, Arnold RS, Guangjie C;

XX WPI: 2000-376545/32.

XX P-PSDB; AAY71121.

XX Protein capable of stimulating superoxide production, useful for treating
XX conditions associated with abnormal growth, including cancer.

PS Claim 4; Page 100-102; 141pp; English.

XX The present sequence is a cDNA encoding rat mitogenic oxidase mox1, also
XX referred as p65mox, which is capable of stimulating production of
XX superoxide, a reactive oxygen intermediate (ROI) that affects cell
XX division. The present sequence was obtained from a rat aortic smooth
XX muscle cell. The mox1 protein functions as a mitogenic regulator and
XX shows homology to human mox1 protein. It is expressed in aortic smooth

KW Rat; mitogenic regulator; mox1B; mitogenic oxidase; p65mox; superoxide;
 KW reactive oxygen intermediate; ROI; cell division; cyostatic;
 KW antipsoriatic; cardiant; antiarteriosclerotic; vasotropic;
 KW antiangiogenic; hypotensive; drug development; treatment; cancer;
 KW abnormal growth; psoriasis; prostatic hypertrophy; proliferation;
 KW blood vessel; lymphatic vessel; benign prostatic hypertrophy;
 KW cardiovascular disease; arteriovenous malformation; eye disorder;
 KW hypertension; atherosclerosis; restenosis; angioplasty; ss.
 XX
 OS Rattus sp.
 XX
 XX Location/Qualifiers
 FH Key 362..1861
 FT CDS /*tag= a
 FT /product= "Mox1B"
 FT /note= "mitogenic oxidase"
 FT polyA_signal 2243..2248
 FT /*tag= b
 FT polyA_signal 2592..2597
 FT /*tag= c
 XX WO200028031-A2.
 XX
 XX 18-MAY-2000.
 XX
 XX 10-NOV-1999; 99WO-US026592.
 XX
 XX 10-NOV-1998; 98US-0107911P.
 PR 17-AUG-1999; 99US-0149332P.
 PR 27-AUG-1999; 99US-0151242P.
 XX
 XX (UYEM-) UNIV EMORY.
 XX
 XX Lambeth JD, Lassegue BP, Griendling KK, Arnold RS, Guangjie C;
 XX WPI; 2000-376545/32.
 DR P-PSDB; AAY71122.
 DR
 XX Protein capable of stimulating superoxide production, useful for treating
 PT conditions associated with abnormal growth, including cancer.
 PT
 XX Claim 4; Page 118-120; 141pp; English.
 XX
 XX The present sequence is a cDNA encoding rat mitogenic oxidase mox1B which
 CC is capable of stimulating production of superoxide, a reactive oxygen
 CC intermediate (ROI) that affects cell division. The present sequence was
 CC obtained from a rat cDNA library constructed in a ZAP express lambda
 CC phage vector using RNA from rat vascular smooth muscle cells exposed to
 CC angiotensin II. Mox1B is a spliced variant of rat mox1, also referred as
 CC p65mox. The mox1B protein functions as a mitogenic regulator. The present
 CC sequence is useful in developing drugs and therapies for treatment of
 CC conditions associated with abnormal growth, including cancer, psoriasis,
 CC prostatic hypertrophy, benign prostatic hypertrophy, cardiovascular
 CC disease, proliferation of vessels, e.g. blood vessels and lymphatic
 CC vessels, arteriovenous malformation, vascular problems associated with
 CC eye, atherosclerosis, hypertension, and restenosis following angioplasty
 XX
 XX Sequence 2619 BP; 692 A; 596 C; 541 G; 790 T; 0 U; 0 Other;
 SQ
 Query Match 45.3%; Score 1182.8; DB 3; Length 2619;
 Best Local Similarity 84.8%; Pred. No. 5.3e-247;
 Matches 1338; Conservative 0; Mismatches 237; Indels 3; Gaps 1;
 347 GTCAACATTGGCTGTGCCGACGCTGTCTCTCTGCTTGAATTTTAAACAGCACGCTGAT 406
 Db 310 GACTGCTTGGCCCTGTGCCAGACATCTGCTTGTGCTGAAATTTTAAACAGCATGTGTAT 369
 407 CTGCTTCTCTGTGTGCGAATCTGCTTCTTCTTCTGAGGGGACCTGCTCATTTTGCAG 466
 Db 370 CTGATTCCTGTGTGCGAATCTGCTCTCTTCTGAGGGGACCTGCTCATTTTGCAG 429
 467 CCGCACACTGAGAAAGCAATTGGATCACACCTCACCTTCCACAGCTGTGSCCTATAT 526

430 CCACACGCTGAGAAAGCCATTGGATCACAACTCACTTCCATAAGCTGTGTGCATATAT 489
 QY 527 GATCTGCCCTACATACAGCTATTACATCATTTGCACACCTCTTTTAACTTTGACTGCTATAG 586
 Db 490 GATCTGCATATTACAGCTATTACATCATTTGCACATCATTTTAACTTTGAAAGCTACAG 549
 QY 587 CAGAACCCAGACAGCCACAGATGGCTCCCTTGGCTCCATCTCTCCAGCCTATCTCATGA 646
 Db 550 TAGAAGCCCAACAGGCCATGGATCTCTTGGCTCTGTCTCTCCAGCCTATTTCCATCC 609
 QY 647 TGAGAAAAGGGGGTCTTGGCTAAATCCCATCCAGTCCGAAACACACAGCTGGAGTA 706
 Db 610 CGAGAAA---GAGATTTTGGCTAAATCCCATCCAGTCTCCAAACGTGACGTGATGTA 666
 QY 707 TGTGACATTCACCCAGCGTTTGGCTCTCACTGGAGTGATCATGACAAATAGCCTTGATTTCT 766
 Db 667 TGCAGCATTTACCAGTATTGCTGGCCCTTACTGGAGTGGTCCGACATGTGGCTTTGGTTCT 726
 QY 767 CATGTAACCTTACGCTACTGAGTTTATCCGGAGAGGTTATTTTGAAGTCTTCTGGTATAC 826
 Db 727 CATGTAACCTTACGCTATGGAGTTTATCCGCGAGGAATTTATTTGAGCTCTTCTGGTATAC 786
 QY 827 TCACCACTTTTATCTTATATCTTGGCTTAGGATTCAGGCAATTCAGGCAATTCGGAATTTGT 886
 Db 787 ACATCACCTTTTATCATCTATATCATCTGCTTAGGATTCATGGCTCTGGGGGGATTTGT 846
 QY 887 CCGGGTCAACAGAGGAGAGCATGAATGAGAGTCACTCTCGCAAGTGTGCGAGTCTTTT 946
 Db 847 CCGGGTCAACAGAGAGAGCATGAGTGAAGTCACTCCCGCAACTGTTTCATACCTTTT 906
 QY 947 TGAGATGTGGATGATCGTGACTCCCACTGTAGGCGCCCTTAAGTTTGAAGGGCATCCCC 1006
 Db 907 CCACGAGTGGGTAAGTATGAAGGAGTTTGCAGGAGTCTCTCAATTTTGTGGGCAACCCCC 966
 QY 1007 TGAGTCTTGGAGTGGATCCTTGACCCGGTCACTTTATATCTGTTGAAGAGATCTCCG 1066
 Db 967 TGGTCTTGGAGTGGATCCTCGCGCGATTCGCTTTTATATCTTTGAAGAGATCTCCG 1026
 QY 1067 GTTTTACCCTCCACAGAGAAGTTGTGATTACCAAGTTTGTATGACCCCATCCAAAGT 1126
 Db 1027 CTTTATCGCTCCCGCAGAGTGTGATTACCAAGTTTGTATGACCCCATGTAAGT 1086
 QY 1127 TTTGAAATGCGATGAACAGAGTGGCTTACGATGGAAGTGGGCGAGTATATCTTTGT 1186
 Db 1087 TTTGAAATGCGATGGAAGAGCGGGCTTTACTATGGAATAGGACAGTATATTTTGT 1146
 QY 1187 TAATTCCTCTCAATCTCTCTCTGGAATGGATCTTTTACTTTGACCTCTGCTCCAGA 1246
 Db 1147 AAATTCCTCTCAATTTCTTCTTCTGGAATGGATCTTTTACTTCTGACCTCTGCTCCAGA 1206
 QY 1247 GGAAGATTTTCTTCTTCTTCCATTCATATCCGAGCAGCGGGAGCTGGACAGAAATCTATAAG 1306
 Db 1207 GGAAGATTTTCTTCTTCCATTCATATTCGAGCAGCGGGAGCTGGACAGAAATCTATAAG 1266
 QY 1307 GCTTTGGAACACAAATATTCACCAATTCGAGGATGAAGTGGATGGTCCCTTGGCAC 1366
 Db 1267 GACATTTGAACACACGACTCCCAATGCCAGGATCGAGTGGATGGTCCCTTGGCAC 1326
 QY 1367 AGCCAGTGGAGTGTTTTCCAGTATGAACTGGCTGTGCTGTTGGAGCAGGAATTCGGGT 1426
 Db 1327 AGTCAGTGGAGTGTCTTCCAGTACGAAGTGGCTGTACTGTTGGGCGAGGATTTGGCGT 1386
 QY 1427 CACCCCTTTGCTTCTTCTTGAATTCATCTGGAATTCATCTGGAATTCAGTGTGCGAGACCAA 1486
 Db 1387 CACTCCCTTTGCTTCTTCTTGAATTCATCTGGAATTCATCTGGAATTCAGTGTGCGAGACCAA 1446
 QY 1487 CTTCAAAAACAAAAGATCTATTTCTATGGAATTCATCTGGAATTCAGTGTGCGAGACCAA 1546
 Db 1447 GCTGAAAACAAAAGATCTATTTCTATGGAATTTTAGAGAGACGGGTGCTTTCCTG 1506
 QY 1547 GTTCAACAACCTTTGACTTCCCTGGAACAGAGATGGAGGAATTAGGCAAGTGGGTTT 1606
 Db 1507 GTTCAACAACCTTTTGAATTTCCCTGGAACAGAGATGGAGGAATTAGGCAACCGGATTT 1566

PR 08-NOV-2000; 2000US-0246528P.
 PR 08-NOV-2000; 2000US-0246532P.
 PR 08-NOV-2000; 2000US-0246609P.
 PR 08-NOV-2000; 2000US-0246610P.
 PR 08-NOV-2000; 2000US-0246611P.
 PR 08-NOV-2000; 2000US-0246613P.
 PR 17-NOV-2000; 2000US-0249207P.
 PR 17-NOV-2000; 2000US-0249208P.
 PR 17-NOV-2000; 2000US-0249209P.
 PR 17-NOV-2000; 2000US-0249210P.
 PR 17-NOV-2000; 2000US-0249211P.
 PR 17-NOV-2000; 2000US-0249212P.
 PR 17-NOV-2000; 2000US-0249213P.
 PR 17-NOV-2000; 2000US-0249214P.
 PR 17-NOV-2000; 2000US-0249215P.
 PR 17-NOV-2000; 2000US-0249216P.
 PR 17-NOV-2000; 2000US-0249217P.
 PR 17-NOV-2000; 2000US-0249218P.
 PR 17-NOV-2000; 2000US-0249244P.
 PR 17-NOV-2000; 2000US-0249245P.
 PR 17-NOV-2000; 2000US-0249264P.
 PR 17-NOV-2000; 2000US-0249265P.
 PR 17-NOV-2000; 2000US-0249297P.
 PR 17-NOV-2000; 2000US-0249299P.
 PR 17-NOV-2000; 2000US-0249300P.
 PR 01-DEC-2000; 2000US-0250160P.
 PR 01-DEC-2000; 2000US-0250391P.
 PR 05-DEC-2000; 2000US-0251030P.
 PR 05-DEC-2000; 2000US-0251988P.
 PR 05-DEC-2000; 2000US-0256719P.
 PR 06-DEC-2000; 2000US-0251479P.
 PR 08-DEC-2000; 2000US-0251856P.
 PR 08-DEC-2000; 2000US-0251868P.
 PR 08-DEC-2000; 2000US-0251869P.
 PR 08-DEC-2000; 2000US-0251989P.
 PR 08-DEC-2000; 2000US-0251990P.
 PR 11-DEC-2000; 2000US-0254097P.
 PR 05-JAN-2001; 2001US-0259678P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Barash SC, Ruben SM;
 XX
 XX WPI; 2001-502630/55.
 DR
 XX Polynucleotides encoding digestive system antigens, useful for
 PT diagnosing, treating, preventing and/or prognosing disorders of the
 PT digestive system, particularly cancer and cancer metastases.
 XX
 PS Disclosure; SEQ ID NO 2637; 986pp; English.
 XX
 CC The present invention provides the protein and coding sequences of a
 CC number of human digestive system antigens. These can be used in the
 CC diagnosis, treatment and prevention of digestive system disorders,
 CC including cancer, Meckel's diverticulum, bacterial or parasitic
 CC infections, appendicitis, Hirschsprung's disease, chronic colitis or
 CC ulcerative colitis. The present sequence is a genomic DNA fragment
 CC encoding a digestive system antigen of the invention
 XX
 SQ Sequence 7517 BP; 2203 A; 1530 C; 1735 G; 2049 T; 0 U; 0 Other;
 Query Match 24.2%; Score 630.6; DB 4; Length 7517;
 Best Local Similarity 91.3%; Pred. No. 7.1e-127;
 Matches 735; Conservative 0; Mismatches 8; Indels 62; Gaps 4;
 QY 1772 CMACTGTGAGTGGAGTTTCTTATGTGCGCCCTCGACTTTGGCAAGAGCGCTGCGCA 1831
 Db 6261 CAGGTCTGTAGTGGAGTTTCTTATGTGCGCCCTCGACTTTGGCAAGAGCGCTGCGCA 6320
 QY 1832 ATGCTGTACCGATATCCAGTCTGGATCCTAGAAAGTTTCAATTCTTACTTCAACAAAGA 1891
 Db 6321 ATGCTGTACCGATATCCAGTCTGGATCCTAGAAAGTTTCAATTCTTACTTCAACAAAGA 6380

QY 1892 AAATTTTTCAGTTATAGGAATAAGGACGGTAATCTGCATTTTGTCTCTTTGTATCTTCAG 1951
 Db 6381 AAATTT-----
 QY 1952 TAATTGAGTTATAGGAATAAGGACGGTAATCTGCATTTTGTCTCTTTGTATCTTCAGTAA 2011
 Db 6387 -----TTGAGTTATAGGAATAAGGACGGTAATCTGCATTTTGTCTCTTTGTATCTTCAGTAA 6443
 QY 2012 TTTACTTGGTCTCNCAGGTTTGANCAGTCACTTTAGGATAAGAAATGTGCTCTCAAGCC 2071
 Db 6444 TTTACTTGGTCTCGTCAGGTTTGAGCAGTCACTTTAGGATAAGAAATGTGCTCTCAAGCC 6503
 QY 2072 TTGACTCCCTGGTATTCCTTTTGGTTCATTCACCTTCGTTTACCTGAGCTTCAGCAAC 2131
 Db 6504 TTGACTCCCTGGTATTCCTTTTGGTTCATTCACCTTCGTTTACCTGAGCTTCAGCAAC 6563
 QY 2132 TTAAGAACTTCTGAAAGTTCCTTAAAGTTCTGAAGTTCTTAAAGCCCATGATCTCTCTCA 2191
 Db 6564 TTAAGAACTTCTGAAAGTTCCTTAAAGTTCTGAAGTTCTTAAAGCCCATGATCTCTCTCA 6623
 QY 2192 GAAAAATACTGTAAATCTTCTGGACAGCCATGACTGTAGCAAGGCTTGTATAGCAGAAG 2251
 Db 6624 GAAAAATACTGTAAATCTTCTGGACAGCCATGACTGTAGCAAGGCTTGTATAGCAGAAG 6683
 QY 2252 TTTGGTGGTTCCANAATTATACAACTAATCCAGGTTTATCAATTCAGTTCAGTGTACCA 2311
 Db 6684 TTTGGTGGTTCCAGAGTTATACAACTAATCCAGGTTTATCAATTCAGTGTACCA 6743
 QY 2312 TCTCTCGAGTTTGGTGTGTAATCTTTGTCTCCACCCACACAGAGATTT-TAAGT 2370
 Db 6744 TCTCTCGAGTTTGGTGTGTAATCTTTGTCTCCACCCACACAGAGATTTCTAAGT 6803
 QY 2371 AGGGTGACTTTTAAATAAAAAATTTATTGAATAATTAATGATAAAACATAATAATAAACA 2430
 Db 6804 AGGGTGACTTTTAAATAAAAAATTTATTGAATAATTAATGATAAAACATAATAATAAACA 6863
 QY 2431 TAAATAATAACAAATTAACCGAAGAACCCCATCCCATTAACACCAACAGTGTACATGT 2490
 Db 6864 TAAATAATAACAAATTAACCGAAGAACCCCATCCCATTAACACCAACAGTGTACATGT 6923
 QY 2491 TTACTGTCACTTTTGATATGGT-TTATCCAGTGTGAACAGCAATTTA---TTATTTTTCG 2546
 Db 6924 TTACTGTCACTTTTGATATGGT-TTATCCAGTGTGAACAGCAATTTTATTTTATTTTTCG 6983
 QY 2547 TCATCAAAAAATAAAGGATTTTTT 2571
 Db 6984 TCATCAAAAAATAAAGGATTTTCTT 7008
 RESULT 9
 AAK87743
 ID AAK87743 standard; cDNA; 1192 BP.
 XX
 AC AAK87743;
 XX
 DT 05-NOV-2001 (first entry)
 XX
 DE Human digestive system antigen coding sequence SEQ ID NO: 59.
 XX
 KW Human; digestive system antigen; gene therapy; cancer; appendicitis;
 KW ulcerative colitis; infection; Hirschsprung's disease; chronic colitis;
 KW digestive system disorder; Meckel's diverticulum; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200155314-A2.
 XX
 XX 02-AUG-2001.
 XX
 PF 17-JAN-2001; 2001WO-US0001324.
 XX
 PR 31-JAN-2000; 2000US-0179065P.
 PR 04-FEB-2000; 2000US-0180628P.

PR 24-FEB-2000; 2000US-0184664P.
 PR 02-MAR-2000; 2000US-0186350P.
 PR 16-MAR-2000; 2000US-0189874P.
 PR 17-MAR-2000; 2000US-0190076P.
 PR 18-APR-2000; 2000US-0198123P.
 PR 19-MAY-2000; 2000US-0205515P.
 PR 07-JUN-2000; 2000US-0209467P.
 PR 28-JUN-2000; 2000US-0214886P.
 PR 30-JUN-2000; 2000US-0215135P.
 PR 07-JUL-2000; 2000US-0216647P.
 PR 07-JUL-2000; 2000US-0216880P.
 PR 11-JUL-2000; 2000US-0217487P.
 PR 11-JUL-2000; 2000US-0217496P.
 PR 14-JUL-2000; 2000US-0218290P.
 PR 26-JUL-2000; 2000US-0220963P.
 PR 26-JUL-2000; 2000US-0220964P.
 PR 14-AUG-2000; 2000US-0224518P.
 PR 14-AUG-2000; 2000US-0224519P.
 PR 14-AUG-2000; 2000US-0225213P.
 PR 14-AUG-2000; 2000US-0225214P.
 PR 14-AUG-2000; 2000US-0225266P.
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 PR 14-AUG-2000; 2000US-0225268P.
 PR 14-AUG-2000; 2000US-0225270P.
 PR 14-AUG-2000; 2000US-0225447P.
 PR 14-AUG-2000; 2000US-0225757P.
 PR 14-AUG-2000; 2000US-0225758P.
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 PR 18-AUG-2000; 2000US-0226279P.
 PR 22-AUG-2000; 2000US-0226681P.
 PR 22-AUG-2000; 2000US-0227182P.
 PR 23-AUG-2000; 2000US-0227009P.
 PR 30-AUG-2000; 2000US-0228924P.
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 PR 05-SEP-2000; 2000US-0229513P.
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 PR 06-SEP-2000; 2000US-0230438P.
 PR 08-SEP-2000; 2000US-0231242P.
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 PR 08-SEP-2000; 2000US-0232080P.
 PR 08-SEP-2000; 2000US-0232081P.
 PR 12-SEP-2000; 2000US-0231968P.
 PR 14-SEP-2000; 2000US-0232397P.
 PR 14-SEP-2000; 2000US-0232398P.
 PR 14-SEP-2000; 2000US-0232399P.
 PR 14-SEP-2000; 2000US-0232400P.
 PR 14-SEP-2000; 2000US-0232401P.
 PR 14-SEP-2000; 2000US-0233063P.
 PR 14-SEP-2000; 2000US-0233064P.
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 PR 21-SEP-2000; 2000US-0234223P.
 PR 21-SEP-2000; 2000US-0234274P.
 PR 23-SEP-2000; 2000US-0234957P.
 PR 26-SEP-2000; 2000US-0235484P.
 PR 27-SEP-2000; 2000US-0235834P.
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 PR 29-SEP-2000; 2000US-0236370P.
 PR 02-OCT-2000; 2000US-0236802P.
 PR 02-OCT-2000; 2000US-0237037P.
 PR 02-OCT-2000; 2000US-0237038P.

PR 02-OCT-2000; 2000US-0237039P.
 PR 02-OCT-2000; 2000US-0237040P.
 PR 13-OCT-2000; 2000US-0239935P.
 PR 13-OCT-2000; 2000US-0239937P.
 PR 20-OCT-2000; 2000US-0240960P.
 PR 20-OCT-2000; 2000US-0241221P.
 PR 20-OCT-2000; 2000US-0241785P.
 PR 20-OCT-2000; 2000US-0241786P.
 PR 20-OCT-2000; 2000US-0241787P.
 PR 20-OCT-2000; 2000US-0241808P.
 PR 20-OCT-2000; 2000US-0241809P.
 PR 20-OCT-2000; 2000US-0241826P.
 PR 01-NOV-2000; 2000US-0244617P.
 PR 08-NOV-2000; 2000US-0246474P.
 PR 08-NOV-2000; 2000US-0246475P.
 PR 08-NOV-2000; 2000US-0246476P.
 PR 08-NOV-2000; 2000US-0246477P.
 PR 08-NOV-2000; 2000US-0246478P.
 PR 08-NOV-2000; 2000US-0246523P.
 PR 08-NOV-2000; 2000US-0246524P.
 PR 08-NOV-2000; 2000US-0246525P.
 PR 08-NOV-2000; 2000US-0246526P.
 PR 08-NOV-2000; 2000US-0246527P.
 PR 08-NOV-2000; 2000US-0246528P.
 PR 08-NOV-2000; 2000US-0246532P.
 PR 08-NOV-2000; 2000US-0246609P.
 PR 08-NOV-2000; 2000US-0246610P.
 PR 08-NOV-2000; 2000US-0246611P.
 PR 08-NOV-2000; 2000US-0246613P.
 PR 17-NOV-2000; 2000US-0249207P.
 PR 17-NOV-2000; 2000US-0249208P.
 PR 17-NOV-2000; 2000US-0249209P.
 PR 17-NOV-2000; 2000US-0249210P.
 PR 17-NOV-2000; 2000US-0249211P.
 PR 17-NOV-2000; 2000US-0249212P.
 PR 17-NOV-2000; 2000US-0249213P.
 PR 17-NOV-2000; 2000US-0249214P.
 PR 17-NOV-2000; 2000US-0249215P.
 PR 17-NOV-2000; 2000US-0249216P.
 PR 17-NOV-2000; 2000US-0249217P.
 PR 17-NOV-2000; 2000US-0249218P.
 PR 17-NOV-2000; 2000US-0249244P.
 PR 17-NOV-2000; 2000US-0249245P.
 PR 17-NOV-2000; 2000US-0249264P.
 PR 17-NOV-2000; 2000US-0249265P.
 PR 17-NOV-2000; 2000US-0249297P.
 PR 17-NOV-2000; 2000US-0249299P.
 PR 17-NOV-2000; 2000US-0249300P.
 PR 01-DEC-2000; 2000US-0250160P.
 PR 01-DEC-2000; 2000US-0250391P.
 PR 05-DEC-2000; 2000US-0251030P.
 PR 05-DEC-2000; 2000US-0251988P.
 PR 06-DEC-2000; 2000US-0256719P.
 PR 06-DEC-2000; 2000US-0251479P.
 PR 08-DEC-2000; 2000US-0251856P.
 PR 08-DEC-2000; 2000US-0251868P.
 PR 08-DEC-2000; 2000US-0251869P.
 PR 08-DEC-2000; 2000US-0251989P.
 PR 11-DEC-2000; 2000US-0251990P.
 PR 11-DEC-2000; 2000US-0254097P.
 PR 05-JAN-2001; 2001US-0259678P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA
 XX
 PI Rosen CA, Barash SC, Ruben SM;
 DR WPI; 2001-502630/55.
 DR P-PSDB; AAM91970.
 XX
 XX
 PT Polynucleotides encoding digestive system antigens, useful for
 PT diagnosing, treating, preventing and/or prognosing disorders of the
 PT digestive system, particularly cancer and cancer metastases.
 XX

PS Claim 1; SEQ ID NO 59; 986pp; English.

XX The present invention provides the protein and coding sequences of a

CC number of human digestive system antigens. These can be used in the

CC diagnosis, treatment and prevention of digestive system disorders,

CC including cancer, Meckel's diverticulum, bacterial or parasitic

CC infections, appendicitis, Hirschsprung's disease, chronic colitis or

CC ulcerative colitis. The present sequence is a cDNA encoding a digestive

CC system antigen of the invention

XX

SQ Sequence 1192 BP; 363 A; 225 C; 193 G; 407 T; 0 U; 4 Other;

Query Match 22.5%; Score 587.6; DB 4; Length 1192;

Best Local Similarity 98.1%; Pred. No. 9.5e-118;

Matches 612; Conservative 1; Mismatches 9; Indels 2; Gaps 2;

QY 1950 AGTAATTGAGTTATAGGAATAAGGACGGTAATCTGCATTTTGTCTTATCTTCAGT 2009

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 2010 AATTACTTGGTCTCMTAGGTTGANCAGTCACTTTAGGATAAGAAATGCGCTCTCAAG 2069

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 119 AATTACTTGGTCTCMTAGGTTGANCAGTCACTTTAGGATAAGAAATGCGCTCTCAAG 178

QY 2070 CCTTGACTCCCTGCTATCTTTTGTATGCACTCAACTTCGTTACTTACGAGTTCAGCA 2129

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 179 CCTTGACTCCCTGCTATCTTTTGTATGCACTCAACTTCGTTACTTACGAGTTCAGCA 238

QY 2130 ACTTAAGAACTTCTGAAGTCTTAAAGTCTTGAANTTCTTAAAGCCCATGGATCCTTTCT 2189

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 239 ACTTAAGAACTTCTGAAGTCTTAAAGTCTTGAAGTCTTAAAGCCCATGGATCCTTTCT 298

QY 2190 CAGAAAAATACTGTAATCTTTCTGCAAGCCATGACTGTAGCAAGGCTTGATAGAGA 2249

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 299 CAGAAAAATACTGTAATCTTTCTGCAAGCCATGACTGTAGCAAGGCTTGATAGAGA 358

QY 2250 AGTTTGGTGTTCANAAATATACAACTAATCCAGGTGATTTTATCAATCCAGTCTTAC 2309

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 359 GGTTCGGTGTTCAGARTTATACAACTAATCCAGGTGATTTTATCAATCCAGTCTTAC 418

QY 2310 CATCTCTCGAGTTTGGTTTGTATCTTTTGTCCCTCCACACCCACAGAGATTTT-TAA 2368

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 419 CATCTCTCGAGTTTGGTTTGTATCTTTTGTCCCTCCACACCCACAGAGATTTTCTAA 478

QY 2369 GTAGGTGACTTTTAAATAAAATTTATGAATAATTAAGATAAAACATAATAATAAA 2428

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 479 GTAGGTGACTTTTAAATAAAATTTATGAATAATTAAGATAAAACATAATAATAAA 538

QY 2429 CATAAATAATAACAAATTTACCGAGAACCCCATCCCATATACACCCACAGGTACAT 2488

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 539 CATAAATAATAACAAATTTACCGAGAACCCCATCCCATATACACCCACAGGTACAT 598

QY 2489 GTTACTGTCACTTTTGATATGTTTATCCAGTGTGAACAGCAATTTATTTTGTCT 2547

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 599 GTTACTGTCACTTTTGATATGTTTATCCAGTGTGAACAGCAATTTATTTTGTCT 658

QY 2548 CATCAAAAAATAAGGATTTTTT 2571

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 659 CATCAAAAAATAAGGATTTTTTCT 682

RESULT 10

ACCC0438

ID ACC00438 standard; DNA; 4266 BP.

XX

XX ACC00438;

XX

XX 07-JUL-2003 (first entry)

DE Human gp91-phox coding sequence, SEQ ID 18.

XX Haemostatic; cytostatic; gene therapy; lentiviral vector; haematopoiesis;

KW lympho-haematological disorder; cancer; haematological cancer; gp91-phox;

KW

gene; ds.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 15..1727

FT /*tag= a

FT /product= "gp91-phox"

XX

PN MO2003029412-A2.

XX

PD 10-APR-2003.

XX

PF 30-SEP-2002; 2002WO-US031023.

XX

PR 02-OCT-2001; 2001US-0326593P.

XX (RERE-) RES DEV FOUND.

XX

PI Trono D, Wiznerowicz M;

XX WPI; 2003-381618/36.

DR P-PSDB; ABR40137.

XX

XX New recombinant lentiviral vector useful in genetic treatments for

PT inherited and acquired lympho-hematological disorders, gene therapies for

PT hematological cancers, and for the study of human hematopoietic stem

PT cells.

XX

PS Example 3; Page 99-103; 105pp; English.

XX

CC The present invention relates to a novel recombinant lentiviral vector

CC (1), comprising: (a) lentiviral gag, pol and rev genes; (b) an expression

CC cassette comprising a transgene positioned under the control of a

CC promoter that is active to promote detectable transcription of the

CC transgene in a human cell; and (c) a central polypurine tract (cPPT;

CC ACC00421) positioned upstream of the expression cassette. (1) is useful

CC in gene therapy for inherited and acquired lympho-haematological

CC disorders, gene therapies for cancers especially haematological cancers,

CC and for the study of haematopoiesis via lentivector-mediated modification

CC of human haematopoietic stem cells. The present sequence is the coding

CC sequence for human gp91-phox. gp91-phox was used as a transgene in the

CC vector of the invention

XX

SQ Sequence 4266 BP; 1242 A; 837 C; 913 G; 1274 T; 0 U; 0 Other;

Query Match 22.3%; Score 582; DB 7; Length 4266;

Best Local Similarity 60.0%; Pred. No. 2.2e-116;

Matches 1035; Conservative 0; Mismatches 665; Indels 24; Gaps 3;

QY 204 ACAATGGGAACTGGGTGGTTAACCACTGGTTTTCAGATTTTGTCTGGTTGTTGTTA 263

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 12 ACCATGGGAACTGGGTGGTTGAATGAGGGCTCTCCATTTTGTCAATCTGGTTGGCTG 71

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 264 GGGCTGAATGTTTCTCTGTTTGGATGCTTCTGAAATATAGAGAGCGGCGCAATAAC 323

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 72 GGGTTGAACGCTCTTCTCTTCTGTTATACCGGGTTTATGATATTCACCTAAGTTT 131

QY 324 TACTACACAAGAAAATCTCTGGTCAACATTTGGCTGTGCCGAGCGTCTGCTCTCTGC 383

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 132 TTTTACACAAGAAAATCTTCTGGTCAACATTTGGCTGTGCCGAGCGGCGCTCTGAGCTGC 191

QY 384 TTGAATTTTACAGCAGCTGATCTCTGCTTCTGTTGTTGCGAATCTGCTCTCTCTG 443

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 192 CTGAATTTCACTGATGCTGATTTCTTTGCGAGTCTGTGGAATCTGCTGCTCTCTCTC 251

QY 444 AGGGCAGCTGCTCAATTTTGCAGCGCCACACTGAGAAAGCAATTGATCACAACCTCAC 503

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 252 AGGGGTTCAGTGCCTGCTCTCAACAGAGTTTCAAGAGCACTGACAGGAAATCTCAC 311

QY 504 TTCCCAAGCTGTCCTATATGATCTGCTTACATACAGCTATTACATCATTCGACAC 563

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 312 TTTTATAAATGGTGGCATGGATGATTGCATTTCACTCTGCGATTTCACACCATTCACAT 371

Qy 564 CTGTTTAACTTTGACTGCTATAGCAGAGCCGACAGGCCACAGATGGCTCCCTTGCCTCC 623
 Db 372 CTATTTTAAATGTTGGAATGGTGTGTGAATGCGAGTCAATAATCTGATTCCTTTATCAAGTA 431
 Qy 624 ATTCTCTCAGCCTATCTCATGATGAGAAAAAGGGGGTCTTGCTTAAATCCCATCCAG 683
 Db 432 GCATCTCTGAACTTGGAGACAGGCAAAATGAAAGTTATCTCAATTTTGCTCGAAAGAGA 491
 Qy 684 TCCCGAAACACGACAGTGG---AGTAGTGACATTCACAGCGTGTGCTCACTGGGA 740
 Db 492 ATAAGAAACCCCTGAAGGAGGCTGTACCTGGCTGTGACCTGTGTCAGGAGGATCACTGGA 551
 Qy 741 GTGATCATGACAATAGCCTGATCTCATGTAATCTCAGTACTCAGTACTGAGTTCAATCGGAGG 800
 Db 552 GTTGTCATCAGCTGTGCTCATATTAATTAATCACTTCTCCACCAAAACCATCCGGAGG 611
 Qy 801 AGTTATTTTGAAGCTCTCTGCTATCTCAGCAGCTTTTATCTTCTATATCTTGGGTTA 860
 Db 612 TCTTACTTTGAAGCTCTTTGGTACACACATCATCTCTTTGTGATCTTCTTCAATGGCCTT 671
 Qy 861 GGAATTCAGGCATTTGTTGAATTTGTCGGGGTCAACAGAGGAGAGCATGAATGAGAGT 920
 Db 672 GCCATCATGAGCTGAACGAATTTGTAAGTGGGAGACCGCAGAGAGTTTGGCTGTGCAT 731
 Qy 921 CATCCTCGCAAGTGTGCAGAGCTCTTTTGAGATGTGGGATGATCGTACTCCACCTGATAGG 980
 Db 732 AATATACAGTTTGTGAACAAAAATCTCAGAAATGGGAAAAATAA---GGAATGCCCA 788
 Qy 981 CGCCTAAGTTTGAAGGCATCCGCCGTGAGTCTTTGGAAGTGGATCCTTGACCCCGTCAAT 1040
 Db 789 ATCCCTCAGTTTGTGGAACCCCTCTATGATCTTGGAAATGATAGTGGTCCCATGTTT 848
 Qy 1041 CTTTATATCTGTGAAGATCCTCGGTTTACCGTCTCCAGCAGAGAGTTGTGATTAAC 1100
 Db 849 CTGTATCTCTGAGAGTTTGTGGGTTTGGGATCTCAACAGAGGTTGTCATACC 908
 Qy 1101 AAGGTGTGTATGCACCCATCAAAAGTTTGGAAATTTGCAGATGAACAAGCGTGGCTCAGC 1160
 Db 909 AAGGTGTCTACTCACCCTTTCAAAACCATCGAGTACAGATGAAGAAGAGGGTTCAAA 968
 Qy 1161 ATGGAAGTGGGCGAGTATATCTTTTAAATGCCCTCAATCTCTCTCTGGAATGGCAT 1220
 Db 969 ATGGAAGTGGGACAATAATTTTGTCAAGTGCCCAAGGTTTCAAGCTGGAGTGGCAC 1028
 Qy 1221 CCTTTTACTTGACCTCTGCTCCAGAGGAAGATTCTTCTCCATTCATATCCGAGCAGCA 1280
 Db 1029 CCTTTTACACTGACATCGCCCCCTTGAGGAAGACTTCTTTAGTATCCATATCCGATCGTT 1088
 Qy 1281 GGGGACTGGACAAAAATCTCATAGGGCTTTTCG-----AACACAA 1322
 Db 1089 GGGGACTGGACAGAGGGGCTGTTCAATGCTTGTGGCTGTGATAGCAGGAGTTTCAAGAT 1148
 Qy 1323 TATTCACCAATTCACGAGTTGAAGTGGATGGTCCCTTTGGCAGAGCCAGTGGAGATGTT 1382
 Db 1149 CGGTGGAACCTACCTAAGATAGCGTTGATGGGCCCTTTGGCACTGCCAGTGAAGATGTG 1208
 Qy 1383 TTCCAGTATGAAGTGGCTGCTGTTGGAGCAGGAATGGGGTCAACCCCTTTGCTTCT 1442
 Db 1209 TTCAGCTATGAGTGGTGGTATTTAGTGGGAGCAGGGATTTGGGTTCACACCCCTTCGCATCC 1268
 Qy 1443 ATCTTGAATCCATCTGTGTAACAAATTCAGTGTGCAGACCAACCTCAAAACAAAAAG 1502
 Db 1269 ATTCTCAAGTCAGTCTGTGTAACAAATTTGCAATAAGCCACCAATCTGAAGCTCAAAAG 1328
 Qy 1503 ATCTATTTCTACTGATCTGAGGAGACAGGTCCTTTTCTGGTCAACAACTGTG 1562
 Db 1329 ATCTACTTCTACTGGCTGTGCCGGGACACACATGCTTTGAGTGGTGTTCAGATCTGCTG 1388
 Qy 1563 ACTTCCCTGGAACAGGAGATGGAGGAATTAGGCAAGTGGGTTTCTTAACTACCGTCTC 1622
 Db 1389 CAATGCTGGAGAGCCAGATGCAGGAAGGAACATGCGCGCTTCTCAGCTACAAATC 1448

Qy 1623 TTCTCACCCTGGGACAGCAATATTCTTGGTCTATGCAGCATTAACCTTTGACAGGCC 1682
 Db 1449 TACCTCACTGCTGGGATGAGTCTCAGGCCAATCACTTGTGTGACCATGATGAGGAG 1508
 Qy 1683 ACTGACATCGTGACAGGTCTGAAACAGAAAAACCTCTCTTTGGGAGACCAATGTGGACAAAT 1742
 Db 1509 AAAGATGTGATCACAGGCTGAAACAAAAGACTTTTGTATGGACGCCCACTGGGATAAT 1568
 Qy 1743 GAGTTTTCTACATAGTACTCTCCACCCCAAGTCTGTAGTGGAGTTTCTTATGTGGC 1802
 Db 1569 GAATTCAGACATTTGCAAGTCAACACCTTAATACCAAGATAGGAGTTTCTCTGTGGA 1628
 Qy 1803 CCTCGGACTTTGGCAAGAGCCTCGCAAAATGCTGCACCATTTCCAGTCTGATCCT 1862
 Db 1629 CCTGAAAGCTTTGGCTGAAACCCCTGAGTAACAAAGCATCTCCAATCTGAGTCTGGCCCT 1688
 Qy 1863 AGAAAGGTTCAATTTCTACTTCAACAAAAGAAAAATTTTTCAGTTAT 1906
 Db 1689 CGGGGAGTGCAATTTCAATTTTCAACAAAGAAAACTTCTAACTGT 1732

RESULT 11

AAS94941

ID AAS94941 standard; DNA; 4324 BP.

XX AAS94941;

AC AAS94941;

XX 14-FEB-2002 (first entry)

XX Human DNA sequence #196 expressed during foam cell differentiation.

XX Human; foam cell differentiation; atherosclerosis; cerebral stroke;

XX cardiovascular disorder; coronary artery disease; gene therapy; ds.

XX Homo sapiens.

XX WO200177389-A2.

XX 18-OCT-2001.

XX 04-APR-2001; 2001WO-US011128.

XX 05-APR-2000; 2000US-C195106P.

XX (INCY-) INCYTE GENOMICS INC.

XX Shiffman D, Somogyi R, Lawn R, Seilhamer JJ, Porter GJ, Mikita T;

XX Tai J;

XX WPI; 2002-010925/01.

XX Composition useful for diagnosis of conditions, disorders or diseases associated with atherosclerosis, comprises several polynucleotides that are differentially expressed in foam cell development.

XX Claim 1; Page 247-248; 315pp; English.

XX The present inventor relates to the isolation of human polynucleotide sequences that are differentially expressed during foam cell differentiation. The polynucleotide sequences of the invention or a composition comprising these polynucleotides are useful as a high throughput method for detecting altered expression of one or more polynucleotides in a sample. The polynucleotides can be used in the diagnosis of disorders associated with foam cell development such as atherosclerosis, cerebral stroke, and cardiovascular disorders such as coronary artery disease. The polynucleotide sequences can also be used as PCR primers and probes. The polynucleotides of the invention are also useful in gene therapy. AAS94746-AAS95021 represent the human polynucleotide sequences of the invention which are differentially expressed during foam cell differentiation

XX Sequence 4324 BP; 1268 A; 843 C; 925 G; 1286 T; 0 U; 2 Other;

	Query Match	22.3%; Score 582; DB 6; Length 4324;
	Best Local Similarity	60.0%; Pred. No. 2.2e-116;
	Matches 1035; Conservative	0; Mismatches 665; Indels 24; Gaps 3;
Qy	204	ACAATGGAAACCTGGGTGTTTAAACCAGTCGGTTTTACGTTTTTGTTTTGTTTCTCGGTGTTGTTGGTTA 263
Dy	59	ACCAATGGGAACCTGGGTGTGAATGAGGGGCTCTCCATTTTGTGCATTCTGTTTTGGCTG 118
Qy	264	GGGCTGAATCTTTTCCCTGTTTGTGGATGTCCTCTCGAAATATGAGAAGGCCGACAAATAC 323
Dy	119	GGGTTGAACGCTTCCTCTTTGTCTGGTAATACGGGGTTTATGATAATCCACTTAAGTTC 178
Qy	324	TACTACACAGAAAAATCCTTTGGGTCAACATTTGGCCGTGTGCCGAGGGTCTGCTCTCTGC 383
Dy	179	TTTTTACACAGAAAACTTTTGGGTACAGCATGGCACTGGCCAGGGCCCCCTGCAGCCCTGC 238
Qy	384	TTGAAATTTTAAACGACGCTGATCCTGTTTCCGTGTGTGTCGCAATCTGCTGTCTCTTCCCTG 443
Dy	239	CTGAAATTTCAACTGCATGCTGAATCTCTTGCCAGTCTGTGAAATCTGCTGTCTCTTCCCTC 298
Qy	444	AGGGCACCTGCTCATTTTTCAGCGCCACACTGAGAAAAGCAATTTGGAATCAAACTCACC 503
Dy	299	AGGGTTCCAGTGGTCTGCTCAACAGAGTTTCCAAGACAACCTGGACAGCAATCTCACC 358
Qy	504	TTCCACAAGCTGGTGGCCCTATGATGTCGCTACATACAGCTATTTACATCATTTGACACAC 563
Dy	359	TTTTCAAAAAATGGTGGCATGGATGATTGCATTTCACTCTCGATTCACACCAATTTGCACAT 418
Qy	564	CTGTTTAACTTTGACTCTATAGCAGAAGCCGACAGCCACAGATGCTCCCTTGCTCTCC 623
Dy	419	CTATTTAATGTGGAATGGTGTGTAATGCCCGAGTCAATAATTCTGAATCTTATTCAGTA 478
Qy	624	ATTCTTCCACGCCATCTCATGATGAAAAAGGGGGTTCTTGGCTTAAATCCCATCCAG 683
Dy	479	GCACTCTCTGAACTTTGGAGACAGCAAAATGAAAGTTATCTCAATTTTGCTCGAAGAGA 538
Qy	684	TCCGAAACACGACAGTGG-- --AGTATGTGACATTTACCAGCGTTGCTGTCTCACTGGA 740
Dy	539	ATAAGAACCTCGAAGGAGCGCTGACTCGCTGTGACCCCTGTTGGCAGGCATCACTGGA 598
Qy	741	GTGATCATGACAATAGCCITTGATTTCTCATGGTAACTTTCACTACTGAGTTTCAATCCGAGG 800
Dy	599	GTGTGTCATACGCTGTGCTCATTAATTAATTAATCACTTCTCCACCAAACCATCCCGAGG 658
Qy	801	AGTTAATTTGAAGTCTTTCTGATATACACACCTTTTATCTCTATATCTCTTGGCTTA 860
Dy	659	TCITTACTTGAAGTCTTTTGGTACACATCACTCTTTGTGATCTTCTTCATTTGGCCTT 718
Qy	861	GGGATTCACGGCAATGTGTGGAATGTCCGGGTCAAAACAGAGGAGACATGAATGAGAT 920
Dy	719	GCCATCCATGGAGCTGAACGAATTTGACGTGGGCAGACCGCAGAGAGTTTGGCTGTGCAT 778
Qy	921	CATCTCGCAAGTGTGCAGAGTCTTTTGAGATGTGGGATGATCGTGACTCCCACTGTAGG 980
Dy	779	AATATAACAGTTTGTGAACAAAAAATCTCAGAATGGGGAATAATAA---GSAATGCCCA 835
Qy	981	CGCCCTAAGTTTGAAGGCACTCCCCCTGAGTCTTTGGAAAGTGATCTTTGACACCGGTCA 1040
Dy	836	ATCCCTCAGTTTGTGGAACCCCTCTGATCTGACTTTGGAAATGGATAGTGGGTCCCAATGTTT 895
Qy	1041	CTTTTATATCTGTAAAGGATCTCTCCGGTTTFAACCGCTCCCAAGCAGAAAGTTGTGATPACC 1100
Dy	896	CTGTATCTCTGTGAGAGTTTGGTGGGTTTTTGGCGATCTCAACAGAAAGTGGTCAATCACC 955
Qy	1101	AAGTTTGTTATGCACCCATCCAAAGTTTTTGGAAATTTGCAGATGAACAGCGTGGCTTCAGC 1160
Dy	956	AAGTGTGTCACTCAACCTTTCAAAACCATCGAGCTACAGATGAAGAAAGAGGGGTTCAAA 1015
Qy	1161	ATGGAAGTGGGGCAGTATCTTTTGTAAATTTGCCCTCAATCTCTCTCTCTCGAATGGCAT 1220
Dy	1016	ATGGAAGTGGGCAATACATTTTGTCAAGTGGCCAAAGGTGTCCAAGCTGGAGTGGCAC 1075
Qy	1221	CTTTTACTTTGACCTCTGCTCCAGAGGAAGATTTCTTCTCAATTCATATCCGAGACGA 1280

XX
PD 27-DEC-2002.
XX
PF 30-MAY-2002; 2002WO-IB004189.
XX
PR 30-MAY-2001; 2001US-0293999P.
PR 22-OCT-2001; 2001US-0330457P.
PR 19-FEB-2002; 2002US-0357144P.
XX
PA (BIOM-) BIOMEDICAL CENT.
XX
PI Baranova AV, Yankovsky NK, Kozlov AP, Lobashev AV, Krukovskaya LL;
XX
DR WPI; 2003-175241/17.
DR P-PSDB; ADAB3895.
XX
PT Determining if a nucleic acid is a marker for a phenotype/cell type of
PT interest, by global comparison of expressed sequence tags known to be
PT expressed in the phenotype/cell type with all ESTs expressed in normal
PT tissue.
XX
PS Claim 23; Page 294; 516pp; English.

XX
XX The invention relates to a novel method for determining if a nucleic acid
CC is a marker for a predetermined phenotype/cell type of interest from a
CC biological species. The method comprises performing a global comparison
CC of a group of expressed sequence tags (ESTs) known to be expressed in the
CC phenotype/cell type of interest with all ESTs expressed in normal tissue
CC in order to identify ESTs that are preferentially expressed in the
CC phenotype/cell type of interest. A method of the invention is useful for
CC determining whether a nucleic acid is a marker for a predetermined
CC phenotype or cell type of interest from a biological species, preferably
CC Arabidopsis or human. The cell type of interest is an abnormal cell such
CC as a tumour cell, and the predetermined phenotype is a stress-induced
CC phenotype such as hyperosmotic stress or high salt conditions. A method
CC of the invention is also useful for determining the progression of colon
CC cancer in a human, for detecting a tumour cell, and for regulating or
CC preventing the growth of a tumour cell. An antibody of the invention is
CC useful for detecting the absence or presence of peptides encoded by
CC tumour-associated markers. A polypeptide of the invention is useful as an
CC immunogen for vaccinating an animal. The present sequence encodes a
CC tumour-associated antigen of the invention.

SQ Sequence 658 BP; 159 A; 168 C; 133 G; 198 T; 0 U; 0 Other;

Query Match 21.1%; Score 551.6; DB 7; Length 658;
Best Local Similarity 97.6%; Pred. No. 5.4e-110;
Matches 560; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 137 GGACCTCTCCAGAAATCCGGATTGCTGAATCTTCCCTGTGCTAGAGGGCTCCAAACCA 196
Db 1 GGACCTCTCCAGAAATCCGGATTGCTGAATCTTCCCTGTGCTAGAGGGCTCCAAACCA 60
QY 197 CCTCTTGACAAATGGGAACTGGGTGGTTAACCACTGGTTTTTCAGTTTGTCTGGTTGT 256
Db 61 CCTCTTGACAAATGGGAACTGGGTGGTTAACCACTGGTTTTTCAGTTTGTCTGGTTGT 120
QY 257 TTGGTTAGGCTGAATGTTTTCCTGTTTGGGATGCTTCTGAAATATGAGAGGCGGA 316
Db 121 TTGGTTAGGCTGAATGTTTTCCTGTTTGGGATGCTTCTGAAATATGAGAGGCGGA 180
QY 317 CAATACTACTACAGAAATAATCTTGGGTCAACATTTGGCTGTGCCGAGGCTCTGC 376
Db 181 CAATACTACTACAGAAATAATCTTGGGTCAACATTTGGCTGTGCCGAGGCTCTGC 240
QY 377 TCTCTGTGTAATTTTAAACAGCAGCTGATCCTCTCTCTGTGTGTGCGCAATCTGCTGC 436
Db 241 TCTCTGTGTAATTTTAAACAGCAGCTGATCCTCTCTCTGTGTGTGCGCAATCTGCTGC 300
QY 437 CTTCCTGAGGGGCACTGCTCATTTTGCAGCGGCACACTGAGAGCAATTTGGATCAAA 496
Db 301 CTTCCTGAGGGGCACTGCTCATTTTGCAGCGGCACACTGAGAGCAATTTGGATCAAA 360

QY 497 CCTCACCTTCCACAAGCTGGTGGCTATATGCTGCTACATACAGCTATTTCACATCAT 556
Db 361 CCTCACCTTCCACAAGCTGGTGGCTATATGCTGCTACATACAGCTATTTCACATCAT 420
QY 557 TGCACACCTGTTTAACTTTGACTGCTATAGCAGAAGCCGACAGGCCACAGATGGCTCCCT 616
Db 421 TGCACACCTGTTTAACTTTGACTGCTATAGCAGAAGCCGACAGGCCACAGATGGCTCCCT 480
QY 617 TGCTCCATCTCTCCAGCCTATCTCATGATGAGAAAAAGGGGGTCTTTGGCTAAATCC 676
Db 481 TGCTCCATCTCTCCAGCCTATCTCATGATGAGAAAAAGGGGGTCTTTGGCTAAATCC 540
QY 677 CATCCAGTCCGAAACACGACAGTGGAGTATG 710
Db 541 CATCCATCCCATATATAACACACAGGTATCATG 574
RESULT 15
AAD00693
ID AAD00693 standard; cDNA; 2044 BP.
XX
AC AAD00693;
XX
DT 08-SEP-2000 (first entry)
XX
DE Human mitogenic regulator mox2 cDNA.
XX
KW Human; mitogenic regulator; mox2; mitogenic oxidase; superoxide;
KW reactive oxygen intermediate; ROI; cell division; cytostatic;
KW antiproliferative; cardiant; antiarteriosclerotic; vasotropic;
KW antiangiogenic; hypotensive; drug development; treatment; cancer;
KW abnormal growth; psoriasis; prostatic hypertrophy; proliferation;
KW blood vessel; lymphatic vessel; benign prostatic hypertrophy;
KW cardiovascular disease; arteriovenous malformation; eye disorder;
KW hypertension; atherosclerosis; restenosis; angioplasty; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 104..1810
FT FT /*tag= a
FT FT /product= "Mox2"
FT FT /note= "mitogenic oxidase"
XX
PN WO200028031-A2.
XX
PD 18-MAY-2000.
XX
PF 10-NOV-1999; 99WO-US026592.
XX
PR 10-NOV-1998; 98US-0107911P.
PR 17-AUG-1999; 99US-0149332P.
PR 27-AUG-1999; 99US-0151242P.
XX
PA (UYEM-) UNIV EMORY.
XX
PI Lambeth JD, Lassegue BP, Griendling KK, Arnold RS, Guangjie C;
XX
DR WPI; 2000-376545/32.
DR P-PSDB; AAY71120.
XX
PT Protein capable of stimulating superoxide production, useful for treating
PT conditions associated with abnormal growth, including cancer.
XX
PS Claim 4; Page 85-89; 141pp; English.
XX
CC The present sequence is a cDNA encoding human mitogenic oxidase mox2
CC which is capable of stimulating production of superoxide, a reactive
CC oxygen intermediate (ROI) that affects cell division. The present
CC sequence was obtained by 5' and 3' RACE techniques using a human foetal
CC kidney cDNA library. The mox2 protein functions as a mitogenic regulator
CC and shows homology to gp91phox protein. It is primarily expressed in
CC foetal tissues with highest expression in foetal kidney. Level of

CC	expression is low in adult tissues. The present sequence is useful in
CC	developing drugs and therapies for treatment of conditions associated
CC	with abnormal growth, including cancer, psoriasis, prostatic hypertrophy,
CC	benign prostatic hypertrophy, cardiovascular disease, proliferation of
CC	vessels, e.g. blood vessels and lymphatic vessels, arteriovenous
CC	malformation, vascular problems associated with eye, atherosclerosis,
CC	hypertension, and restenosis following angioplasty
XX	
SQ	Sequence 2044 BP; 540 A; 502 C; 476 G; 526 T; 0 U; 0 Other;
	Query Match 20.0%; Score 521.2; DB 3; Length 2044;
	Best Local Similarity 57.4%; Pred. No. 3e-103;
	Matches 1012; Conservative 0; Mismatches 723; Indels 27; Gaps 3;
Qy	202 TGCAAAATGGGAAACATGGGTGGTTAAACACATGGTTTTCAGTTTGTGTTCTGTTGTTGGT 261
Db	
Qy	102 TCATGATGGGGTCTGGATTTTGAATGAGGGTCTCTCCACCATATTAGTACTCTCATGGC 161
Db	
Qy	262 TAGGCTGGAATGTTTTCTGTTTGTGATGCGCTTCTGAAATATGAAAGCGCGACAAT 321
Db	
Qy	162 TGGGAAATAAATTTTATCTGTTTATTGACACGTTCTACTGTATGAAAGAGGAGGAGTCTT 221
Db	
Qy	322 ACTACTACACAGAAAAATCCTTGGGTCAACATTTGGCTGTGCCGAGCCCTGCTCTCT 381
Db	
Qy	222 TCCATTTACACAGAGTTATTTTGGGTTTCAACATCTGGCTTGGGACGAGCATCCGACTGT 281
Db	
Qy	382 GCTTGAATTTTAAACAGACGCTATCCTGCTCTGTGTGCGCAATCTGCTGCTCTTC 441
Db	
Qy	282 GCCTGAATTTTAACTGATGCTAATTTCTAATACCTGTGCTGNAACCTTATTTCATTC 341
Db	
Qy	442 TGAGGGGCACCTGCTCTATTTTTCAGCCGCGACACTGAGAAAGCAATTGGATCACAACCTCA 501
Db	
Qy	342 TAAGAGGAAACAAGTATTTTGTCTGACAGAGGACCGTGGAGAGGCAATTAGACAAAAACCTCA 401
Db	
Qy	502 CCTTCCACAGCTGGTGGCTATATGATCTGCCTACATACAGCTATTTCATCATTTGCAC 561
Db	
Qy	402 GATTTCACAACTGGTTCGCCCTATGGGATAGCTGTTAATGCAACCATCCACATCGTGGCGC 461
Db	
Qy	562 ACCTGTTTAACTTTGACTGCTATAGCAGAAGCCACAGGCCACACAGATGGCTCCCTTCGCT 621
Db	
Qy	462 ATTTCTTCACTTGGAAAGCTTACACTTGGAGCCAGTCCGAGGAGGCCAGGAGACTTCTGG 521
Db	
Qy	622 CCATTTCTCTCCAGCCTATCTCATGATGAGAAAAAGGGGGTTCTTGGCTAAATCCCATCC 681
Db	
Qy	522 CCGCACTTTTCCAGCTGGGCAACACCCCTTAACGAGAG-----CTACCTCAACCCCTGCTC 575
Db	
Qy	682 AGTCCCGAAACACGACAGTGGAGTATGTGACATTCACAGGGTTGTCTGTTCTACTGGAG 741
Db	
Qy	576 GGAACCTTTCCCCACAAACACAACTGAATTGCTAAGGACAATAGCAGGGGTACCGGTC 635
Db	
Qy	742 TGATCATGACAAATAGCCTTGATTTCTCATGTTAACTTCAGCTACTGAGTTCATCCGAGGA 801
Db	
Qy	636 TGGTGATCTCTCTGGCTTTTAGCTTTTGAATCATGACCTCGTCAACTGAGTTTCATCAGCAG 695
Db	
Qy	802 GTTATTTTGAAGTCTTCTGTFATACTCACCACTTTTTTATCTTCTATATCCTTGGCTTAG 861
Db	
Qy	696 CCTCCTATGAGTTGTTCTCTGTTACACACCATGTTTTTCATCGTCTCTTCTCAGCCTGG 755
Db	
Qy	862 GGATTCAGGCATTTGGTGGAAATTTGTCGGGGTCAACACAGAGGAGCATGATGAGAGTC 921
Db	
Qy	756 CCATCCATGGGACGGGTCGGAATTTTCGAGGCCAAACCCAAGACAGTCTCTCTCTGCACA 815
Db	
Qy	922 ATCCTCGCAAGTGTGCAGAGTCTTTTGAGATGTCGGATGATCGGTGACTCCCACTGTAGGC 981
Db	
Qy	816 ACATCACCTTCTGTAGAGACCGCTATGCAGATGG---CHAGACAGTGGCCCAATGCCCCG 872
Db	
Qy	982 GCCCTAAGTTTGAAGGGCATCCCCCTGAGTCTTGGAAAGTGGATCCTTTGCACCGGTCAATC 1041
Db	
Qy	873 TGCCTCAATTTTCTGGCAAGGAAACCTTCGGCTTGGAAATGGATTTTAGGCCCTGTGGTCT 932
Db	
Qy	1042 TTTATATCTGTGAAGGATCTCCGGTTTTTACCGCTCCGACGAAAGTTGTGATTACCA 1101
Db	
Qy	933 TGTATGCACTTGTGAAGAATAATATTAGTTCTGGCAATTTCAACAAGAAGTTGTCAATTACCA 992
Db	

Qy	1102	AGTTGTATTGCAACCATCCAAAGTTTGGAAATGCGAGTAGCAACAGCGTGGCTTCAGCA	1161
Db	993	AGGTGGTAAGCCACCCTCTGGAGTCTCTGAACTTCACATGAAAAAGCGTGGCTTTAAAA	1052
Qy	1162	TGGAAGTGGGGCAGTATATCTTTGTAAATTTGCCCTCAATCTCTCTCGATGGATCGCATC	1221
Db	1053	TGGCGCAGGGCAGTATCATCTTGGTGCAGTGCACCAATATCTTCGCTGGATGGCACC	1112
Qy	1222	CTTTTATCTTTGACCTCTGCTCCAGAGAGAAATTTCTTCCATTCATPATCCGAGCAGCAG	1281
Db	1113	CTTTCACCTTCACTCTGCCCCCAGGAAGACTTTTTCAGCGTGCAATCCGGGCAACAG	1172
Qy	1282	GGACTGGACAGAAAATCTCATAGGCGCTTT-----CGAACAACAAT	1323
Db	1173	GAGACTGGACAGCAGCGCTACTCGAGCGCTTTTGGGGCAGAGGACAGGCCCTCCAGGAGC	1232
Qy	1324	ATTACCAATTTCCAGGATTTGAAGTGGATGGTCCCTTTTGGCAGCAGCAGTGAGGATGTTT	1383
Db	1233	CCTGGAGCCTGCCAAGCGCTGGCAGTGGACGGGCCCCTTTGGAACTGGCCCTGACAGATGAT	1292
Qy	1384	TCCAGTATGAAGTGGCTGTCTGGTTGGAGCAGGAATTTGGGGTCACCCCCTTTGCTTCTA	1443
Db	1293	TTCACTACCCAGTGTGTGTGGTGTGCCCGGGGATCGAGTCACTCCCTTCGTGCTC	1352
Qy	1444	TCCTGAAATCCATCTGTGTACAAATTCACAGTGTGGAGACCAACCTCAAAACAAAAGA	1503
Db	1353	TTCTGAAATCTATATGGTACAAATGCAAGTGAGGACAGACCCCACTGAAGCTGAGCAAGG	1412
Qy	1504	TCATTTCTTACTGATCTGCAGGAGACAGTGCCTTTTCTCGTTTCAACAACTGTGTA	1563
Db	1413	TGATTTTCTACTGGATTTGCCGGGATGCAAGAGCTTTTGAGTGGTTGTGTGATCTCTTAC	1472
Qy	1564	CTTCCCTGGAAACAGGAGATGGAGGAATTAGGCAAAAGTGGGTTTTTCTAAAATAACCGTCTCT	1623
Db	1473	TCTCCCTGGAAACACGGATGAGTGAGCAGGGGAAACTCACTTTCTGAGTTATCATATAT	1532
Qy	1624	TCCTCACCGGATGGGACAGCAATATTGTGGTCAATGACGACATTAACATTTTGAACAAGGCCA	1683
Db	1533	TTCTTACCGCTGGGATGAAATACAGGCTCTTCACATAGCTTTTACACTGGGACGAAATA	1592
Qy	1684	CTGCATCTGTGCAGGCTTGAAACAGAAAACCTCCCTTTGGGAGACCAATGTGGGACAAATG	1743
Db	1593	CTGACGTGATTCAGGCTTTAAGCAGAAGACCTTCTATGGGAGGCCCAACTGGAAACAATG	1652
Qy	1744	AGTTTTTCTACAATAGTACCTCCCAACCCCAAGTCTGTAGTGGGAGTTTTTCTTATGTGCCC	1803
Db	1653	AGITCAAGCAGATTGCCTACAATCACCCACAGCAGCATATGGCGTGTCTTCTGTGAC	1712
Qy	1804	CTCGACTTTGGCAAGAGCCTGGCAAAATGTGTGTCAACCGAATATCCAGTCTGGATCCTA	1863
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Qy	1864	GAAAGTTCAATTTCTACTTCAACAAAGAAATTTTTCAGTTATAGGAATTAAGGACGGTAA	1923
Db	1773	GAGTGTTCATTTCTATTACAACAAGAGAGCTTCTAGACTTTTGGAGTCAAGTCCAGGC	1832
Qy	1924	TCGTCAATTTTGTCTCTTTGTAT	1945
Db	1833	ATTGTGTTTCAATCAAGTTAT	1854

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OM nucleic - nucleic search, using sw model

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB	ID	Description
1	2605	99.8	2609	4	US-09-437-568A-1	Sequence 1, Appli
2	1305	50.0	2577	4	US-09-437-568A-22	Sequence 22, Appl
3	1182.8	45.3	2619	4	US-09-437-568A-41	Sequence 41, Appl
4	579.4	22.2	4267	4	US-09-023-655-1379	Sequence 1379, Ap
5	521.2	20.0	2044	4	US-09-437-568A-3	Sequence 3, Appli
6	206	7.9	206	4	US-09-023-655-292	Sequence 292, App
7	66.8	2.6	3453	4	US-09-437-568A-47	Sequence 47, Appl
8	65	2.5	5494	4	US-09-437-568A-45	Sequence 45, Appl
9	55.6	2.1	6070	4	US-10-204-708-10	Sequence 10, Appl
10	53.8	2.1	832	4	US-09-621-976-2813	Sequence 2813, Ap
11	52.8	2.0	19124	2	US-08-487-826B-13	Sequence 13, Appl
12	52.6	2.0	817	3	US-08-885-469-1	Sequence 1, Appli
13	52.6	2.0	817	4	US-09-625-918-1	Sequence 1, Appli
14	51.2	2.0	3680	4	US-09-647-390-15	Sequence 15, Appl
15	51	2.0	6326	4	US-10-204-708-57	Sequence 57, Appl
16	51	2.0	7304	4	US-10-204-708-44	Sequence 44, Appl
17	50.8	1.9	2745	4	US-09-833-381-1410	Sequence 1410, Ap
18	50.8	1.9	5852	1	US-07-867-106-2	Sequence 2, Appli
19	50.8	1.9	9347	4	US-10-204-708-35	Sequence 35, Appl
20	50.2	1.9	1420	2	US-08-909-9650-3	Sequence 3, Appli
21	50.2	1.9	3581	2	US-08-738-349-1	Sequence 1, Appli
22	50.2	1.9	11049	4	US-10-204-708-24	Sequence 24, Appl
23	50	1.9	640681	4	US-09-790-988-1	Sequence 1, Appli
24	49.2	1.9	396	4	US-09-640-173-10	Sequence 10, Appl
25	49.2	1.9	396	4	US-09-713-550-10	Sequence 10, Appl
26	49.2	1.9	780	4	US-09-454-279-17	Sequence 17, Appl
27	48.8	1.9	1215	4	US-09-220-132-184	Sequence 184, App

28	48.8	1.9	2116	4	US-08-635-552A-1	Sequence 1, Appli
29	48.8	1.9	3736	2	US-08-480-473B-1	Sequence 1, Appli
30	48.8	1.9	3736	3	US-08-915-213-1	Sequence 1, Appli
31	48.8	1.9	3736	3	US-09-148-547-1	Sequence 1, Appli
32	48.8	1.9	3736	3	US-09-235-217-1	Sequence 1, Appli
33	48.8	1.9	3736	4	US-09-383-581-1	Sequence 1, Appli
34	48.8	1.9	3736	5	PCT-US96-10251-1	Sequence 1, Appli
35	48.8	1.9	4055	4	US-09-620-312D-706	Sequence 706, App
36	48.8	1.9	5152	4	US-10-204-708-48	Sequence 48, Appl
37	48.4	1.9	5501	4	US-10-204-708-38	Sequence 38, Appl
38	48.2	1.8	239	4	US-09-621-976-16632	Sequence 16632, A
39	48	1.8	1937	4	US-09-647-143-1	Sequence 1, Appli
40	47.8	1.8	5562	4	US-10-204-708-63	Sequence 63, Appl
41	47.8	1.8	11131	4	US-10-204-708-27	Sequence 27, Appl
42	47.6	1.8	554	4	US-09-696-169A-14	Sequence 14, Appl
43	47.4	1.8	296	2	US-09-032-684-13	Sequence 13, Appl
44	47.4	1.8	296	4	US-09-644-460-13	Sequence 13, Appl
45	47.4	1.8	1883	4	US-09-149-476-170	Sequence 170, App

ALIGNMENTS

RESULT 1
US-09-437-568A-1
; Sequence 1, Application US/09437568A
; Patent No. 6620603
; GENERAL INFORMATION:
; APPLICANT: Lambeth, J. David
; APPLICANT: Griending, Kathy
; APPLICANT: Lassegue, Bernard
; APPLICANT: Arnold, Rebecca S.
; APPLICANT: Cheng, Guangjie
; TITLE OF INVENTION: No. 6620603el Mitogenic Regulators
; FILE REFERENCE: 05501-0103
; CURRENT APPLICATION NUMBER: US/09/437,568A
; CURRENT FILING DATE: 1999-11-10
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2609
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (2025)
; OTHER INFORMATION: n at position 2025 = any nucleotide
; NAME/KEY: modified_base
; LOCATION: (2036)
; OTHER INFORMATION: n at position 2036 = any nucleotide
; NAME/KEY: modified_base
; LOCATION: (2164)
; OTHER INFORMATION: n at position 2164 = any nucleotide
; NAME/KEY: modified_base
; LOCATION: (2264)
; OTHER INFORMATION: n at position 2264 = any nucleotide
; NAME/KEY: CDS
; LOCATION: (207)..(1901)
US-09-437-568A-1

Query Match 99.8%; Score 2605; DB 4; Length 2609;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2609; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	121	ATGTTCCATTCTCGAAGGACCTCTCCAGANTCCGGATGCTGGAATCTTCCCTGTTGCCTTA	180

[illegible]

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Db	1261	CCATTCATATCCGAGCAGCAGGGGA	CTGGACAGAAAATCTCATAAAGGGCTTT	CGAAACAAC	1320	
Qy	1321	AATATTCACCAATTC	CCAGGATTTGAAGTGGA	TGGTCCCTTTGGCA	CAGCAGTGGAGATG	1380
Db	1321	AATATTCACCAATTC	CCAGGATTTGAAGTGGA	TGGTCCCTTTGGCA	CAGCAGTGGAGATG	1380
Qy	1381	TTTTTCCAGTATGAAGTGGCTG	CTGCTGTTGGACAGGAATTTGGGGT	CACCCCTTTGCTT	1440	
Db	1381	TTTTTCCAGTATGAAGTGGCTG	CTGCTGTTGGACAGGAATTTGGGGT	CACCCCTTTGCTT	1440	
Qy	1441	CTATCTTGAATCCATCT	TGGTACAAATTC	CCAGTGTGCAGACAC	CAACCTCAAAACA	1500
Db	1441	CTATCTTGAATCCATCT	TGGTACAAATTC	CCAGTGTGCAGACAC	CAACCTCAAAACA	1500
Qy	1501	AGATCTATTTCTACT	CGAGTCGAGGAGACAGTGCCTTTTCCCTGGT	TTCAACAACCTCT	1560	
Db	1501	AGATCTATTTCTACT	CGAGTCGAGGAGACAGTGCCTTTTCCCTGGT	TTCAACAACCTCT	1560	
Qy	1561	TGACTTCCCTCGGAACAGGAGAT	GGAGGAATTAGGCAAAAGTGGT	TTTTCTTAACTACCGTC	1620	
Db	1561	TGACTTCCCTCGGAACAGGAGAT	GGAGGAATTAGGCAAAAGTGGT	TTTTCTTAACTACCGTC	1620	
Qy	1621	TCTTCTC	CCAGGATGGGACAGCAATATTTGGTGCAT	GCAGCATTAACATTTGACAAG	1680	
Db	1621	TCTTCTC	CCAGGATGGGACAGCAATATTTGGTGCAT	GCAGCATTAACATTTGACAAG	1680	
Qy	1681	CCACTGACATCTGTGACAGGCT	CTGAAACAGAAAACCTCCTTTGGGAGACCAAT	TGGGACA	1740	
Db	1681	CCACTGACATCTGTGACAGGCT	CTGAAACAGAAAACCTCCTTTGGGAGACCAAT	TGGGACA	1740	
Qy	1741	ATGAGTTTTTCTACAATAGCTA	CTCTCCACCCCAAGTCTGTAGTGGAGTTTTCTTATGTG	1800		
Db	1741	ATGAGTTTTTCTACAATAGCTA	CTCTCCACCCCAAGTCTGTAGTGGAGTTTTCTTATGTG	1800		
Qy	1801	GCCTCGGACTTTGGCAAGAGGCT	CGCAATGCTCACCAGATATCCAGTCTGGATC	1860		
Db	1801	GCCTCGGACTTTGGCAAGAGGCT	CGCAATGCTCACCAGATATCCAGTCTGGATC	1860		
Qy	1861	CTAGAAAGGTTCAATTTCTACT	TTCAACAAAGAAAATTTTGAGTTATAGGAATAAGGACGG	1920		
Db	1861	CTAGAAAGGTTCAATTTCTACT	TTCAACAAAGAAAATTTTGAGTTATAGGAATAAGGACGG	1920		
Qy	1921	TAATCTGCATTTTGTCTCTTTGTATCTT	CAGTAAATGAGTTATAGGAATAAGGACGGTAA	1980		
Db	1921	TAATCTGCATTTTGTCTCTTTGTATCTT	CAGTAAATGAGTTATAGGAATAAGGACGGTAA	1980		
Qy	1981	CTCTGCATTTTGTCTCTTTGTATCTT	CAAGTAAATTTACTTGGTCTCCTCAGTTTGANCAGT	2040		
Db	1981	CTCTGCATTTTGTCTCTTTGTATCTT	CAAGTAAATTTACTTGGTCTCCTCAGTTTGANCAGT	2040		
Qy	2041	CACTTTAGATAGAAATGCTCTC	CAAGCTTGACTCCCTGGTATCTTTTTTTTGATG	2100		
Db	2041	CACTTTAGATAGAAATGCTCTC	CAAGCTTGACTCCCTGGTATCTTTTTTTTGATG	2100		
Qy	2101	CATTCAACTTCGTTATCTT	CGACTTCAGCAACTTAAGAACTCTGAAGTTCTTAAAGTTCT	2160		
Db	2101	CATTCAACTTCGTTATCTT	CGACTTCAGCAACTTAAGAACTCTGAAGTTCTTAAAGTTCT	2160		
Qy	2161	GAANTTCTTAAACCCCAT	TGGAATCTTTCTCAGAAAATAAATCTGTAAATCTTTTCTGACAG	2220		
Db	2161	GAANTTCTTAAACCCCAT	TGGAATCTTTCTCAGAAAATAAATCTGTAAATCTTTTCTGACAG	2220		
Qy	2221	CCATGACTGTAGCAAGCTTGA	TAGCAGAGTTTGGTGGTCTCANAAATTAACAACCTAATC	2280		
Db	2221	CCATGACTGTAGCAGGCTTGA	TAGCAGAGTTTGGTGGTCTCANAAATTAACAACCTAATC	2280		
Qy	2281	CCAGGTGAATTTATCAATTC	CAAGTGTATCCATCTCTGAGTTTTGGTTTTGTAATCTTTTG	2340		
Db	2281	CCAGGTGAATTTATCAATTC	CAAGTGTATCCATCTCTGAGTTTTGGTTTTGTAATCTTTTG	2340		

Db 1490 GAACAGAGATGGACGATTAAGGCAAAACCGGATTTCTTAACCTACCGACTCTTCTCACT 1549
Qy 1632 GGATGGACAGCAATATTTGTTGGTTCATGCAAGCAATTAACCTTTGCAAGGCCACTGCAATC 1691
Db 1550 GGCTGGGATAGCAACATTTGCTGGTTCATGCAAGCAATTAACCTTTGCAAGGCCACTGCAATC 1609
Qy 1692 GTGACAGGCTGGAACAGAAACCTCTTTGGGAGACCAATGTTGGGACCAATGAGTTTCT 1751
Db 1610 CTGACAGGCTGGAACAGAAACCTCTTTGGGAGACCAATGTTGGGACCAATGAGTTTCT 1669
Qy 1752 ACAATAGTACTCTCCCAACCCCAAGCTGTAGTGGGAGTTTCTTTATGTTGGCCCTCGACT 1811
Db 1670 AGAATAGTACTCTCCCAACCCCAAGCTGTGTGGGGTTTCTTTATGCGGCCCTCGACT 1729
Qy 1812 TTGGCAAGAGCCTGGGCAAAATGTTGCAACGATATTCAGTCTGGATCCCTAGAAAGTT 1871
Db 1730 TTGGCAAAAGCCTGGGCAAAATGTTGCAACGATATTCAGTCTGGATCCCTAGAAAGTT 1789
Qy 1872 CAATTCTACTTCAACAAAGAAATTTTGTAGTTATAGGAATAAGACGGTAAT 1924
Db 1790 CAATTCTACTTCAACAAAGAAACGTTCTGAATTTGGAGGAGCCGCAACAGTAGT 1842

RESULT 3
; Sequence 41, Application US/09437568A
; Patent No. 6620603
; GENERAL INFORMATION:
; APPLICANT: Lambeth, J. David
; APPLICANT: Griendling, Kathy
; APPLICANT: Lassegue, Bernard
; APPLICANT: Arnold, Rebecca S.
; APPLICANT: Cheng, Guangjie
; TITLE OF INVENTION: No. 6620603el Mitogenic Regulators
; FILE REFERENCE: 05501-0103
; CURRENT APPLICATION NUMBER: US/09/437,568A
; CURRENT FILING DATE: 1999-11-10
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 41
; LENGTH: 2619
; TYPE: DNA
; ORGANISM: Rat
US-09-437-568A-41

Query Match 45.3%; Score 1182.8; DB 4; Length 2619;
Best Local Similarity 84.8%; Pred. No. 4.6e-296;
Matches 1338; Conservative 0; Mismatches 237; Indels 3; Gaps 1;
Qy 347 GTCACATTTGGCTGTGCCGAGGCTCTGCTCTGCTTGAATTTTAAACAGCAGCTGAT 406
Db 310 GACTGCTTGGCTTGGCCAGAGCAATCTGCTTGTGCTGAAATTTTAAACAGCATGGTAT 369
Qy 407 CTTGCTTCTGTGTGCAATCTGCTCTCTCTCTCTGAGGGGCACTGCTCATTTTGGAG 466
Db 370 CTTGATTCCTGTGTGCAATCTGCTCTCTCTCTGAGGGGCACTGCTCATTTTGGAA 429
Qy 467 CGGCACTGGAAGAAATTTGGATCAAACTGACCTTCCCAAGCTGGTGGCCATAT 526
Db 430 CCACACGCTGGAAGAAATTTGGATCAAACTGACCTTCCCAAGCTGGTGGCCATAT 489
Qy 527 GATCTGCTACATACAGCTATTTCATCATATTGCAACCTGTTTAACTTTGACTGTATAG 586
Db 490 GATCTGATATTTCACAGCTATTTCATATCATTTGCAATCTATTAACTTTGACGCTACAG 549
Qy 587 CAGAACCCGACAGGCCACAGATGGCTCCCTTTGCCCTCAATCTCTCCAGCTATCTCATGA 646
Db 550 TAGAAGCCCAACAGGCCATGATGGATCTCTTGGCTCTGTTCTCTCCAGCTATTCCATCC 609
Qy 647 TGAGAAAAGGGGGTTCTTGGCTAAATCCCATCAGTCCCGAAACACAGCAGTGGATGA 706
Db 610 CGAGAAA---GAAGATTTCTTGGCTAAATCCCATCAGTCTCCAAAACGTCGACAGTATGTA 666

Qy 707 TGTGACATTCACACGCGTTGCTGTCTCACTGGAGTGTATCATGACAATAGCTCTTGATCT 766
Db 667 TGCAGCATTTACAGTATTTGCTGCGCTTACTGGAGTGGTCCCACTGTGGCTTTGGTTCT 726
Qy 767 CATGGTAACTTACGCTACTGAGTTTCATCCGAGGAGTTATTTTGAAGTCTTTCTGSTATAC 826
Db 727 CATGGTAACTTACGCTACTGAGTTTATCCCGCAGGAATTTATTTGAGCTTCTCTGGTATAC 786
Qy 827 TCACACCTTTTATCTTTATATCTTCTTGGCTTGGGATTCACGGCATTTGTTGGAATTTGT 886
Db 787 ACATCACCTTTTATCTATCTATATCATCTGCTTAGGGATCCATGCGCTGGGGGGGATTTGT 846
Qy 887 CCGGGGTCAACACAGGAGAGCATGAATGAGAGTCACTCTCGCAAGTGTGACAGAGTCTTT 946
Db 847 CCGGGGTCAACACAGGAGAGCATGAGTGAAGTCACTCCCGCAACTGTTTCATACTCTTT 906
Qy 947 TGAGATGTGGGATGATCGTCACTCCCACTGTAGGCGCCCTAAGTTTGAAGGCAATCCCCC 1006
Db 907 CCACGAGTGGGATAAGTATGAAGGAGTTGCGAGGAGTCTCATTTTGTGGGGCAACCCCC 966
Qy 1007 TGAGTCTTGGAGTGGATCTTTCACCGGTCAATTTCTTTATATCTGTGAAAGGATCCCTCG 1066
Db 967 TGAGTCTTGGAGTGGATCTTTCGCGCGGATTTGCTTTTATATCTTTGAAGGATCTTTCTG 1026
Qy 1067 GTTTTACCGCTCCGACGAGAGGTTGTGATTACCAAGGTTGTTATGACCCCATCCAAAGT 1126
Db 1027 CTTTATTCGCTCCCGCAGAGGTCGTGATTACCAAGGTTGTCATGACCCCATGTAAAGT 1086
Qy 1127 TTTGGAATTTGCAATGAACAAAGCGTGGCTTCAGCATGTGAAGTGGGGCAGTATATCTTTGT 1186
Db 1087 TTTGGAATTTGCAATGAAGAAAGCGGGCTTTACTATGGAATAGGACAGTATATATCTGT 1146
Qy 1187 TAATTGGCCCTCAATCTCTCTCGGAATGCACTCTTTACTTTGACTCTGCTGCCAGA 1246
Db 1147 AAATTGGCCCTCGAATTTCCCTTCCGGAATGCACTCTTTACTCTGACTCTGCTGCCAGA 1206
Qy 1247 GGAAGATTTCTTCTCCATTCATATCCGACAGCAGGGGACCTGGACAGAAAATCTCATAG 1306
Db 1207 GGAAGATTTTCTCCATTCATATCGACAGCAGGGGACCTGGACAGAAAATCTCATAG 1266
Qy 1307 GGGTTTCGAACACAAATANTCCAAATTCACAGATTCAGGATGAAGTGAAGTGTCTTTGGCAC 1366
Db 1267 GACATTTGAACACAGCACTCACCAATGCCAGGATCGAGGTGAGTGTCTTTGGCAC 1326
Qy 1367 AGCAGTGGAGATGTTTCCAGTATGAGTGTGCTGTGCTGTGGAGCAGAAATTTGGGCT 1426
Db 1327 AGTCAGTGGAGATGTTTCCAGTACGAAGTGGCTGTACTGTTGGGGCAGGATTTGGCT 1386
Qy 1427 CACCCCTTTGCTTCTATCTTTGAAATCCATCTGGTACAAAATTCAGAGTGTGACAGACCAA 1486
Db 1387 CACTCCCTTTGCTTCTTTGAAATCTATCTGGTACAAAATTCAGAGCTGACACACAA 1446
Qy 1487 CTTCAAAACAAAAGATCTATTTCTACTGATCTGAGGGAGACAGTGTGCTTTTCTGT 1546
Db 1447 GCTGAAAACACAAAAGATCTATTTCTACTGATTTGTAGAGAGACGGGTGCTTTGCTGT 1506
Qy 1547 GTTCAACAAACCTTGTGACTTCCCTGGAACAGAGATGGAGAAATTTAGGCAAAAGTGGT 1606
Db 1507 GTTCAACAACTTATTTGAATTCCTTGGAAACAGAGATGGACGAAATTTAGGCAAAACCGGAT 1566
Qy 1607 TCTAACTACCGTCTCTTTCTCTCACGGATGGGACAGCAATATTTGTTGTCATGACAGATT 1666
Db 1567 CTTAACTACCGACTCTTCTCTCACTGGCTGGGATAGCAACATTTGCTGTCTATGACGACT 1626
Qy 1667 AAACTTTGCAAGGCCACTGATCGTGCAGAGTCTGAAACAGAAAACCTCTCTTTGGGAG 1726
Db 1627 AAACCTTTGACAGGCACTGACGCTCTGCAAGGCTGGAACAGAAAACCTCTCTTTGGGAG 1686
Qy 1727 ACCAATGTGGGCAATGAGTTTCTTCAAAATAGTACTCTCCCAACCCCAAGTCTGTAGTGG 1786
Db 1687 ACCAATGTGGGCAATGAGTTTCTTGAATAGTACTTGCACCCCAAGTCTGTGTGG 1746
Qy 1787 AGTTTCTTATGTGCCCCTCGACTTTTGGCAAGAGCCTGTGGCAAAATGTGTCAACGATA 1846

Db 1747 GGTTCCTTAATGCGCCCTCCGACTTTGGCAAAAGGCTGGCAATGCTGCGCGTA 1806
Qy 1847 TTCAGTCTGATCTAGAAAGTTCAATCTACTTCAACAAAGAAATTTTCAGTTAT 1906
Db 1807 CTCAGTCTGATCTAGAAAGTTCAATCTACTTCAACAAAGAAAGTTTCTGAATGG 1866
Qy 1907 AGGAATAGGACGGTAAT 1924
Db 1867 AGGAGCGCACAGTAGT 1884

RESULT 4

US-09-023-655-1379
; Sequence 1379, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION NUMBER: US/09/023,655
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1379:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4267 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g37983
US-09-023-655-1379

Query Match 22.2%; Score 579.4; DB 4; Length 4267;
Best Local Similarity 60.0%; Pred. No. 7.6e-140;
Matches 1033; Conservative 0; Mismatches 666; Indels 24; Gaps 3;

Qy 205 CAATGGAAACTGGGTGTTAAACCACTGGTTTTCAGTTTGTCTGTTGTTGTTAG 264
Db 14 CATCGGGAACTGGGCTGTGAATGAGGGCTCTCCATTTTGTCTATCTGTTTGGCTGG 73
Qy 265 GCGTGAATCTTTCCTGTTTGGATGCGCTTCTGAAATATGAGAGCGCCGCAAAATCT 324
Db 74 GGTGAAACGCTCTTCTCTTTGTCTGTTATACGGGGTTTATGATATTCACCTAAGTTCT 133

Qy 325 ACTACACAAGAAATCCTTTGGGTCAACATTTGGCCTGTGCCGAGCGCTGTCTCTCTGCT 384
Db 134 TTATACACAAGAAATCCTTTGGGTCAACATTTGGCCTGTGCCGAGCGCTGTCTCTCTGCT 193
Qy 385 TGAATTTTAAACACGACCTGATCTCTGCTTCTGTGTGTGTCGAATCTGTCTCTCTCTGA 444
Db 194 TGAATTTTAAACACGACCTGATCTCTTGTGTCAGTCTGTGAAATCTGTCTCTCTCTCTCA 253
Qy 445 GGGGACCTCTCTCATTTTTCAGCGCCACACATGAGAAAGCAATTTGGATCACAACCTCACCT 504
Db 254 GGGGTTCCAGTGGGTCTCTCAACAGAGTTTGAAGACAACTGGGACAGAATCTCACCT 313
Qy 505 TCACAAGCTGGTGGCCTATATGATCTGCCTACATACAGCTATTTCAATCTTTCGACACACC 564
Db 314 TTCAATAAATGGTGGCATGGATGATTCACCTTCACTCTGCGATTTCACACCATTCGACATC 373
Qy 565 TGTTTAACTTTGACTGCTATAGCAGAAAGCCGACAGGCCACAGATGGTCTCCCTGGCTCCA 624
Db 374 TATTTAATGTGGAATGGTGTGTAATGCCCGAGTCAATTAATCTGTATCTTATTCAGTAG 433
Qy 625 TTCTCTCCAGCCTATCTCATGATGAGAAAGGGGGTTCCTTGGCTAAATCCCACATCCAGT 684
Db 434 CACTCTCTGNACTTGGAGACAGGCAAAATGAAAGTTTATCTCAATTTTGTCTGAAAGAGAA 493
Qy 685 CCGAAACACGACAGTGG---AGTATGTGACATTTCAACAGCGTTGCTGTCTCACTGGAG 741
Db 494 TAAAGAACCTGAAAGGAGGCTGTACCTGTGCTGTGACCTGTTGGCAGGCATCACTGGAG 553
Qy 742 TGATCATGACATAGCCTTGAATCTCATGTAACTTCAGTCTAGTCTAGTCTATCCGAGGA 801
Db 554 TTGTCAACGCTGTGCTCATATTAATTAATCACTTCTCCACCAAAACCATCCGAGGT 613
Qy 802 GTTATTTTGAAGTCTTCTGTATCTACACACCTTTTATCTTCTATATCTTGGCTTAG 861
Db 614 CTTACTTTGAAGTCTTTTGGTACACATCACTCTTGTGTGATCTTCTTCAATTTGGCCTTG 673
Qy 862 GGAATCACGGCATTTGGTGAATTTCCGGGGTCAACACAGAGGAGCATGAATGAGATC 921
Db 674 CCATCCATGGAGCTGAACGAATTTGTACGTGGGACAGCCGACAGAGTTTGGCTGTGATA 733
Qy 922 ATCCTCGCAAGTGTGCAGAGTCTTTTGAGATGTGGGATGATGTGATCTCCCATCTAGGC 981
Db 734 ATATAACAGTTTGTGAACAAAAAATCTCAGAATTTGGGAAAAAATAAA---GGAATGCCCAA 790
Qy 982 GCCCTAAGTTTGAAGGGCATCCCTCTGAGTCTTGAAGTGGATCTCTTGACACCGTCATTC 1041
Db 791 TCCCTCAGTTTGTGAAACCTCTCTATGACTTGGAAATGGAATAGTGGGTCCCATGTTTC 850
Qy 1042 TTTATATCTGTGAAGAGATCTCCCGGTTTACCGCTCCACAGCAGAGAGTTGTGATTAACA 1101
Db 851 TGTATCTCTGTGAGAGGTTGTGCGGTTTGGCGATCTCAACAGAAGTGGTTCATCACCA 910
Qy 1102 AGGTTGTTATGACCCATCCAAAGTTTGGAAATTCAGATGCAACAGCGTGGTTCAGCA 1161
Db 911 AGGTGTCTACTCACCTTTCAAAAACATCGAGCTACAGATGAAGAAGAGGGGTTCAAAA 970
Qy 1162 TGGAAAGTGGGCGAGTATATCTTTGTGTTAATTTGCCCTCAATCTCTCTCTGGAAATGCAATC 1221
Db 971 TGGAAAGTGGGCAATACATTTTGTCAAGTGGCCCAAGAGTGTCCAAGCTGGAGTGGCACCC 1030
Qy 1222 CTTTATCTTTGACCTCTGCTCCAGAGGAGATTTCTTCTTCCATTCATATCCGAGCAGCAG 1281
Db 1031 CTTTATACATGACATCCGCGCTCTGAGGAAGACTTCTTTAGTATTCATATCCGATCGTTG 1090
Qy 1282 GGGACTGACGACGAAATCTCATAAGGGCTTTCG-----AACAAAT 1323
Db 1091 GGGACTGACGACGAGGGGCTGTTCATGCTGTGGCTGTGTAAGCAGGAGTTTCAAGATG 1150
Qy 1324 ATTCAACCAATTTCCAGGATTTGAAGTGGATGTTCCCTTTGGCACACCGCAGTGAAGTATTT 1383
Db 1151 CGTGGAAACTACCTAAGATAGCGGTTGATGGCCCTTTGGCAGCTGCCAGTGAAGATGTT 1210
Qy 1384 TCCAGTATGAAGTGTCTGTGTTGGAGCAGGAATTTGGGGTTCACCCCTTTTGTCTTA 1443


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Db 1293 TTCACTACCCAGTGTGTGTGCGTTGCCGGGATCGAGTCACTCCCTTCGTGTC 1352
Qy 1444 TCTTGAATCCATCTGGTACAAATTCACAGTGTGCAGACCAACCTCAAAACAAAAAGA 1503
Db 1353 TCTCGAAATCATATGTGTACAAATGCAGTGAAGGACAGACCCCACTGAAGCTGAGCAGG 1412
Qy 1504 TCTATTTCTACTGATCTGCAGGAGAGACAGGTGCTTTCTCTGTTCAACACCTGTGA 1563
Db 1413 TGTATTTCTACTGATTTGCCGGATGCAAGAGCTTTTGTGGTTGCTGATCTCTTAC 1472
Qy 1564 CTTCCTCTGGAACAGAGATGAGGAAATTAGGCAAGTGGGTTTCTAACTACCGTCTCT 1623
Db 1473 TCTCCTCTGGAACACCGGATGAGTGAGCAGGAGGAACTCACTTCTGTGTTATCATAT 1532
Qy 1624 TCCTCAGCGATGGACAGACGATATTGTGTGATGAGCAATTAACCTTTGACAGGCCA 1683
Db 1533 TCTTACCGGCTGGATGAAATCAGGCTCTTCATAGCTTTACACTGGGACGAAATA 1592
Qy 1684 CTGACATCGTGACAGGTCTGAAACAGAAACCTCTTTGGGAGACCAATGTGGACAATG 1743
Db 1593 CTGACGTGATTACAGGCTTAAAGCAGAGACCTTCTATGGAGGCCCACTGGACAATG 1652
Qy 1744 AGTTTCTCAATAGTACCTCCACCCCAAGTCTGTAGTGGAGTCTTCTTATGTGCC 1803
Db 1653 AGTTCAAGCAGATTGCCATAATCAATCAACCCAGCAGTATTGGGTCTTCTGTGGAC 1712
Qy 1804 CTGGGCTTTGGCAAGAGCCTGGGCAATGTGTGACCGATATCCAGTCTGGATCCTA 1863
Db 1713 CTAAAGCTCTCTGAGGACACTTCAAAAGATGTGCCACTTGTATTATCATAGCTGACCCCA 1772
Qy 1864 GAAAGGTTCAATTTCTACTCAACAAAGAAATTTTGGATATAGNATAGGACGGTAA 1923
Db 1773 GAGGTGTTCAATTTCTATTACAAAGAGAGCTTCTAGACTTTGGAGGTCAAGTCCAGG 1832
Qy 1924 TCTGCAATTTGCTCTTTGAT 1945
Db 1833 ATGTGCTTTTCAATCAAGTTAT 1854
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RESULT 6
US-09-023-655-292
; Sequence 292, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSER: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
```

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;
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 292:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 206 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: COLNUT03
; CLONE: 1341948
; US-09-023-655-292
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Query Match 7.9%; Score 206; DB 4; Length 206;
Best Local Similarity 100.0%; Pred. No. 6.9e-44;
Matches 206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 881 AATTGTCCGGGTCAACACAGAGAGCATGAATGAGATCATCTCGCAAGTGTGAGA 940
Db 1 AATTGTCCGGGTCAACACAGAGAGCATGAATGAGATCATCTCGCAAGTGTGAGA 60
Qy 941 GTCTTTGAGATGTGGATGATCGTGACTCCCACTGTAGCGCCCTAAGTTTGAAGGCA 1000
Db 61 GTCTTTGAGATGTGGATGATCGTGACTCCCACTGTAGCGCCCTAAGTTTGAAGGCA 120
Qy 1001 TCCCTCTGAGTCTTGAAGTGGATCCTTGACCGGTCAATCTTTATATCTGTGAAAGAT 1060
Db 121 TCCCTCTGAGTCTTGAAGTGGATCCTTGACCGGTCAATCTTTATATCTGTGAAAGAT 180
Qy 1061 CTCTCCGTTTACCGCTCCCGCAGA 1086
Db 181 CTCTCCGTTTACCGCTCCCGCAGA 206
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RESULT 7
US-09-437-568A-47
; Sequence 47, Application US/09437568A
; Patent No. 6620603
; GENERAL INFORMATION:
; APPLICANT: Lambeth, J. David
; APPLICANT: Griendling, Kathy
; APPLICANT: Lassegue, Bernard
; APPLICANT: Arnold, Rebecca S.
; APPLICANT: Cheng, Guangjie
; TITLE OF INVENTION: No. 6620603el Mitogenic Regulators
; FILE REFERENCE: 05501-0103
; CURRENT APPLICATION NUMBER: US/09/437,568A
; CURRENT FILING DATE: 1999-11-10
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 47
; LENGTH: 3453
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (438)..(3134)
; US-09-437-568A-47
```

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Query Match 2.6%; Score 66.8; DB 4; Length 3453;
Best Local Similarity 49.0%; Pred. No. 2.9e-07;
Matches 247; Conservative 0; Mismatches 242; Indels 15; Gaps 2;

Qy 1024 TCCTTGACCGGTCACTTTATATCTGTGAAGATCCTCCGGTTTACCGCTCCAGC 1083
Db 2239 TCCTGGTCCCGCAATCATCTATGGAGTGACAGCTGCTGAGCCGGAAGAGG 2298
Qy 1084 AGAAGTTGTGATTACCAAGTGTATTATGCAACCATCAAAAGTTTGGAAATGAGATGA 1143
Db 2299 TGGAGATCAGCGTGTGAAGCGGAGCTGTGCTCCCTCAGGAGTGACCTACCTGCAATTC 2358
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QY	1144	ACAAG---CGTGGCTTCAGCATGGAAGTGGGCGAGTATATCTTTGTTAAATGGCCCTCAA	1200
Db	2359	AGAGGCCCAAGGCTTTGAGTACAGTCAGACAGTGGGTGGGATCGCTGGCTC	2418
QY	1201	TCTCTCTCCTGGGAATGGCATCCCTTTTACTTTGACCTCTGCTCCAGAGGAAGATTTCTTCT	1260
Db	2419	TGGGGACACCGAGTACACGCCCTTCACACTGACCTCCGGGCCCATGAGGACACACTCA	2478
QY	1261	CCATTATATCCGAGCAGCAGGAGCTGGACAGAAATCTCATAGGCGCTTTGAAACAAC	1320
Db	2479	GCCTGACATCCGGGCGAGTGGGCCCTGGACCACTCCCTCAGGAGATCTACTCATCCC	2538
QY	1321	AAAT-----TTACCAATCCAGGATCCAGGATGGAATGATGGTCCCTTTGGGCACAG	1368
Db	2539	CAAGGGCAATGGCTGTCTGGATACCAAGAGCTGTACCTTGATGGACCGTTTGGAGAGG	2598
QY	1369	CCAGTGAGGATGTTTCCAGTATGAAGTGGCTGTGGTGGTGGAGCAGGAATGGGGTCA	1428
Db	2599	GCCATCAGGAGTGGCATAAAATTTGAGGTGTCAAGTGTGGTGGGAGGGGGCAATGGGGTCA	2658
QY	1429	CCCCCTTTGCTCTATCTTTGAAATCCATCTGGTACAAATCCAGTGTGCAGACCAACAAC	1488
Db	2659	CCCCCTTTGCTCTATCTTTGAAATCCATCTGGTACAAATCCAGTGTGCAGACCAACAAC	1488
QY	1489	TCAAAACAAAAAAGATCTATTCT	1512
Db	2719	TGTGTAGAAGATCTACTTCACT	2742
RESULT 8			
US-09-437-568A-45			
; Sequence 45, Application US/09437568A			
; Patent No. 6620603			
; GENERAL INFORMATION:			
; APPLICANT: Lambeth, J. David			
; APPLICANT: Griendling, Kathy			
; APPLICANT: Lassegue, Bernard			
; APPLICANT: Arnold, Rebecca S.			
; APPLICANT: Cheng, Guangjie			
; TITLE OF INVENTION: No. 6620603el Mitogenic Regulators			
; FILE REFERENCE: 05501-0103			
; CURRENT APPLICATION NUMBER: US/09/437,568A			
; CURRENT FILING DATE: 1999-11-10			
; NUMBER OF SEQ ID NOS: 61			
; SOFTWARE: PatentIn Ver. 2.0			
; SEQ ID NO 45			
; LENGTH: 5494			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: (155)..(4810)			
US-09-437-568A-45			
Query Match 2.5%; Score 65; DB 4; Length 5494;			
Best Local Similarity 49.9%; Pred. No. 1.1e-06;			
Matches 229; Conservative 0; Mismatches 215; Indels 15; Gaps 2;			
QY	1024	TCCTTGCACCGCTATCTTTATATCTGTGAAGGATCTCCGGTTTATCCGCTCCACGC	1083
Db	3912	TCTGTCTCCAGCAATCATCTATGTTGGGGCGACAAGCTGGTGGAGCTGAGCCGCGAGAAGG	3971
QY	1084	AGAAGGTTGTGATTAACAAGTTGTTTATGACCCCAATCCAAAGTTTGGAAATGCGATGA	1143
Db	3972	TGGAGATCAGCGTGGTGAAGCGGAGCTGCTGCCCTCAGAGTGACCCACCTGCGGTCC	4031
QY	1144	ACAAG---CGTGGCTTCAGCATGGAAGTGGGCGAGTATATCTTTGTTAAATGGCCCTCAA	1200
Db	4032	AGCGGCCCAAGGCTTTGAGTACAAGTCAGGCGAGTGGGTGGGATCGCTTGGCTGGCTC	4091
QY	1201	TCTCTCTCTCGGAATGCAATCTTTTACTTTTACCTCTGCTCCAGAGGAAGATTTCTTCT	1260
RESULT 9			
US-10-204-708-10/c			
; Sequence 10, Application US/10204708			
; Patent No. 6677731			
; GENERAL INFORMATION:			
; APPLICANT: OLEK, Alexander			
; APPLICANT: PIEPENBROCK, Christian			
; APPLICANT: BERLIN, Kurt			
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication			
; TITLE OF INVENTION: by Assessing DNA Methylation			
; FILE REFERENCE: 5013.1c12			
; CURRENT APPLICATION NUMBER: US/10/204,708			
; CURRENT FILING DATE: 2003-05-06			
; PRIOR APPLICATION NUMBER: PCT/EP01/03971			
; PRIOR FILING DATE: 2001-04-06			
; PRIOR APPLICATION NUMBER: DE 10019058.8			
; PRIOR FILING DATE: 2000-04-05			
; PRIOR APPLICATION NUMBER: DE 10019173.8			
; PRIOR FILING DATE: 2000-04-07			
; PRIOR APPLICATION NUMBER: DE 10032529.7			
; PRIOR FILING DATE: 2000-06-30			
; PRIOR APPLICATION NUMBER: DE 10043826.1			
; PRIOR FILING DATE: 2000-09-01			
; NUMBER OF SEQ ID NOS: 98			
; SEQ ID NO 10			
; LENGTH: 6070			
; TYPE: DNA			
; ORGANISM: Artificial Sequence			
; FEATURE:			
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)			
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Query Match 2.1%; Score 55.6; DB 4; Length 6070;			
Best Local Similarity 53.2%; Pred. No. 0.0003;			
Matches 118; Conservative 0; Mismatches 104; Indels 0; Gaps 0;			
QY	2398	AAAAATTTATTAATAATTAATGATAAAACATAATAATAAAATAATAATAATAACAAAT	2447
Db	1906	ACAAACAATTTCTTTTAAATAATAAAATTTCTAAATAATAATAATAATAATAAT	1847
QY	2448	TACCGAGAACCCATCCCCATATAACACACAGTGTACATGTTTACTGTCTACTTTGAT	2507
Db	1846	TTCAACAACAATATAATAATATCTTAATACCAATAAACTATACACTTAAAAATAATAAT	1787
QY	2508	ATGGTTTATCCAGTGTGAACAGCAATTTATTTTTCCTCATCAAAAAATAAAGGATTT	2567
Db	1786	TATATTAATAATAATTTTATCAACACACAAAAAAAACAAAAACGAAAAAATAA	1727
QY	2568	TTTTTTCACCTGAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	2609
Db	1726	AAAAAATAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	1685
RESULT 10			


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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/885,469
; FILING DATE:
; APPLICATION NUMBER: US/08/885,469
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Sprunger, Suzanne A.
; REGISTRATION NUMBER: P-41,323
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8284
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 817 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; MOLECULE TYPE: cdna
; US-08-885-469-1

Query Match 2.0%; Score 52.6; DB 3; Length 817;
Best Local Similarity 75.3%; Pred. No. 0.00066;
Matches 61; Conservative 3; Mismatches 17; Indels 0; Gaps 0;

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Db 737 GRAAMTAATGTTAGTCGMAAATAAAGTTTTTTTTWTWAAAAA 796

QY 2589 AAAAAA 2609
Db 797 AAAAAA 817

US-09-625-918-1
;
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 817 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; MOLECULE TYPE: cdna
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
; US-09-625-918-1

Query Match 2.0%; Score 52.6; DB 4; Length 817;
Best Local Similarity 75.3%; Pred. No. 0.00066;
Matches 61; Conservative 3; Mismatches 17; Indels 0; Gaps 0;

QY 2529 GCAATTTATTATTTTGGCTCATCAAAATAAAGGATTTTTTTTCACCTTGAAAAA 2588
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QY 2589 AAAAAA 2609
Db 797 AAAAAA 817

US-09-647-390-15
;
; GENERAL INFORMATION:
; APPLICANT: Stuiver, Maarten
; APPLICANT: Simons, Lambertus
; TITLE OF INVENTION: Pathogen-Inducible Promoter
; FILE REFERENCE: MCG 5:707/UST
; CURRENT APPLICATION NUMBER: US/09/647,390
; CURRENT FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: EP 98201024.1
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: PCT/EP99/02178
; PRIOR FILING DATE: 1999-03-25
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 3680
; TYPE: DNA
; ORGANISM: Helianthus annuus
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(1889)
; NAME/KEY: CDS
; LOCATION: (1890)..(3503)
; US-09-647-390-15

Query Match 2.0%; Score 51.2; DB 4; Length 3680;
Best Local Similarity 52.9%; Pred. No. 0.0032;
Matches 110; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

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QY 2461 ATCCCCATATAACACCAACAGTGATGTTTACTGTCTACATTTTGTGATGTTTAT 2520
Db 751 GTAGCGAGTAAAGTTATGATGTTTCTAACTTTTATGTTTCTTATTTCTATCTGTT 810

QY 2521 TGTGAACGCAATTTATTTTGTCTCATCAAAATAAAGGATTTTTTTTCACCTTGA 2580
Db 811 AATATATATAAAGATAAAGGAGTTGGTAAACCAATAATATAAAGAGTTGGTTAAAG 870

QY 2581 AAAAAA 2608
Db 871 AAAAAA 898

RESULT 14
US-09-647-390-15
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; Sequence 15, Application US/09647390
; Patent No. 6465836
; GENERAL INFORMATION:
; APPLICANT: Stuiver, Maarten
; APPLICANT: Custers, Jerome
; APPLICANT: Simons, Lambertus
; TITLE OF INVENTION: Pathogen-Inducible Promoter
; FILE REFERENCE: MCG 5:707/UST
; CURRENT APPLICATION NUMBER: US/09/647,390
; CURRENT FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: EP 98201024.1
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: PCT/EP99/02178
; PRIOR FILING DATE: 1999-03-25
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 3680
; TYPE: DNA
; ORGANISM: Helianthus annuus
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(1889)
; NAME/KEY: CDS
; LOCATION: (1890)..(3503)
; US-09-647-390-15

Query Match 2.0%; Score 51.2; DB 4; Length 3680;
Best Local Similarity 52.9%; Pred. No. 0.0032;
Matches 110; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

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QY 2461 ATCCCCATATAACACCAACAGTGATGTTTACTGTCTACATTTTGTGATGTTTAT 2520
Db 751 GTAGCGAGTAAAGTTATGATGTTTCTAACTTTTATGTTTCTTATTTCTATCTGTT 810

QY 2521 TGTGAACGCAATTTATTTTGTCTCATCAAAATAAAGGATTTTTTTTCACCTTGA 2580
Db 811 AATATATATAAAGATAAAGGAGTTGGTAAACCAATAATATAAAGAGTTGGTTAAAG 870

QY 2581 AAAAAA 2608
Db 871 AAAAAA 898
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RESULT 15
US-10-204-708-57/c
; Sequence 57, Application US/10204708
; Patent No. 6677731
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of diseases Associated with DNA Replication
; FILE REFERENCE: 5013.1012
; CURRENT APPLICATION NUMBER: US/10/204,708
; CURRENT FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: PCT/EP01/03971
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 57
; LENGTH: 6326
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-204-708-57

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Query Match	2.0%;	Score 51;	DB 4;	Length 6326;
Best Local Similarity	53.8%;	Pred. No. 0.0047;		
Matches 105;	Conservative	0;	Mismatches 90;	Indels 0;
QY	2414	AAACATATATATAACATATAATATAACAAAATTACCGAGACCCGATCCCATATAAC	2473	
Db	3447	ABAAATACAAAAATTACCTAAATATAATAATACCTATAATCCCACTACTTTAAAAA	3388	
QY	2474	ACCAACAGTGTCATGTTTACTCTGCATCTTTTGATATGGTTTTATCCAGTGGACACGAAT	2533	
Db	3387	ACTAAAAACATAAAAAATCGCTCGAACTCAAAAAATAAAATTACAATAACCGAAATCAT	3328	
QY	2534	TTATATTTTTTGCTCATCAAAAATAAAGGATTTTTTTCACCTGAAAAAIAAAAAAAAAA	2593	
Db	3327	CTATTACACTCCAACTTATACACAAAGAAACTCCATCTCAACAAAAAIAAAAAAAAAA	3268	
QY	2594	AAAAAAAAAAAAAAAAA	2608	
Db	3267	AAAAAAAAAAAAAAAAA	3253	

Search completed: July 23, 2004, 13:28:39
Job time : 315 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 23, 2004, 08:30:25 ; Search time 1142 Seconds
(without alignments)

11167.752 Million cell updates/sec

Title: US-10-618-839-1

Perfect score: 2609

Sequence: 1 gctgatagcacagtctctgc.....aaaaaaaaaaaaaaaaaaaaa 2609

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3216467 seqs, 244149694 residues

Total number of hits satisfying chosen parameters: 6432934

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2605	99.8	2609	13	US-09-878-722-244
2	2605	99.8	2609	13	US-09-904-456-244
3	2605	99.8	2609	15	US-10-157-031-174
4	2605	99.8	2609	15	US-10-318-906A-1
5	2605	99.8	2609	15	US-10-319-236A-1
6	2605	99.8	2609	15	US-10-393-590-13
7	2605	99.8	2609	15	US-10-393-567-13
8	2605	99.8	2609	17	US-10-618-839-1
9	1305	50.0	2577	15	US-10-318-906A-22
10	1305	50.0	2577	15	US-10-319-236A-22
11	1182.8	45.3	2619	15	US-10-318-906A-41
12	1182.8	45.3	2619	15	US-10-319-236A-41
13	797	30.5	797	17	US-10-618-839-15
14	582	22.3	4266	13	US-10-342-887-480

15	582	22.3	4266	13	US-10-172-118-480	Sequence 480, App
16	582	22.3	4266	13	US-10-418-036-1	Sequence 1, Appli
17	582	22.3	4266	15	US-10-261-078-18	Sequence 18, Appl
18	582	22.3	4324	15	US-10-240-965-196	Sequence 196, App
19	579.4	22.2	4267	15	US-10-171-581-257	Sequence 257, App
20	579.4	22.2	4267	17	US-10-641-643-1379	Sequence 1379, Ap
21	551.6	21.1	658	15	US-10-157-031-175	Sequence 175, App
22	521.2	20.0	2044	9	US-09-999-248-6	Sequence 6, Appli
23	521.2	20.0	2044	13	US-10-418-036-5	Sequence 5, Appli
24	521.2	20.0	2044	15	US-10-318-906A-3	Sequence 3, Appli
25	521.2	20.0	2044	15	US-10-319-236A-3	Sequence 3, Appli
26	521.2	20.0	2044	17	US-10-618-839-3	Sequence 5, Appli
c	521.2	20.0	2044	17	US-10-618-839-5	Sequence 5, Appli
27	511.8	19.6	531	15	US-10-066-543-3290	Sequence 3290, Ap
28	501.2	19.2	560	12	US-09-969-034-1969	Sequence 1969, Ap
29	496.8	19.0	509	15	US-10-066-543-2589	Sequence 2589, Ap
c	479.2	18.4	503	15	US-10-225-486-34	Sequence 34, Appl
32	478.6	18.3	555	9	US-09-878-178-519	Sequence 519, App
33	478.6	18.3	555	14	US-10-046-935-519	Sequence 519, App
34	478.6	18.3	555	15	US-10-146-502-519	Sequence 519, App
c	468.6	18.0	491	13	US-09-878-722-227	Sequence 227, App
c	468.6	18.0	491	13	US-09-904-456-227	Sequence 227, App
c	460.4	17.6	562	12	US-09-969-034-1885	Sequence 1885, Ap
38	460.4	17.6	570	9	US-09-878-178-1857	Sequence 1857, Ap
39	460.4	17.6	570	14	US-10-046-935-1857	Sequence 1857, Ap
40	460.4	17.6	570	15	US-10-146-502-1857	Sequence 1857, Ap
41	445	17.1	446	9	US-09-878-178-1774	Sequence 1774, Ap
42	445	17.1	446	14	US-10-046-935-1774	Sequence 1774, Ap
43	445	17.1	446	15	US-10-146-502-1774	Sequence 1774, Ap
44	423.6	16.2	579	12	US-09-969-034-1500	Sequence 1500, Ap
45	418	16.0	586	12	US-09-969-034-2527	Sequence 2527, Ap

ALIGNMENTS

RESULT 1

US-09-878-722-244
; Sequence 244, Application US/09878722
; Publication No. US20020040127A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuguu
; APPLICANT: Hepler, William T.
; APPLICANT: Clapper, Jonathan
; APPLICANT: Wang, Aijun
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.524
; CURRENT APPLICATION NUMBER: US/09/878,722
; CURRENT FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 245
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 244
; LENGTH: 2609
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(2609)
; OTHER INFORMATION: n = A,T,C or G
US-09-878-722-244

Query Match 99.8%; Score 2605; DB 13; Length 2609;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2609; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

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Db

1 GCTGATAGCACAGTCTCTGTCAGAGAGGCGGCGGAATAAACTTATTTCATTCACAGAA 60
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QY

61 CTCITGGGGTAGGTGTGTGTTTTTCATCTTAAGGCTCACAGACCTGCGCTGCAGAA 120
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1621	Qy	TCCTTCCTCACCGGATGGGACAGCAATATTTGGTTCATGCAGGATTAACACTTTGACAAGG	1680
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1681	Qy	CCACTGCATCGTCACAGGTCCTGAAAACAGAAAAACCTCTTTGGGAGACCAATGTGGGACA	1740
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1741	Qy	ATGAGTTTTCTTACAATAGTACCTCCCAACCCCAAGTCTGTAGTGGAGTTTTCTTATGTG	1800
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1921	Qy	TAAATCTGAATTTGTCTCTTTGTATCTTCAGTAATTGAGTTATAGGAATAAGACCGTTAA	1980
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1981	Qy	TCTGCATTTTCTCTTTGTATCTTCAGTAATTTTACTTTGTCTCTNTCAGGTTTGANCAGT	2040
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2101	Qy	CAATTCAACTTGGTTACTTTGAGCTTCACCACTTAAGAACTCTGAGTTCCTTAAAGTTCT	2160
2101	Db	CAATTCAACTTGGTTACTTTGAGCTTCACCACTTAAGAACTCTGAGTTCCTTAAAGTTCT	2160
2161	Qy	GAANTTCTTAAAGCCCATGGATCCCTTCTCAGAAAAATAACTGTAAATCTTCTCTGGACAG	2220
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2221	Qy	CCATGACTGTAGCAAGGCTTGATAGCAGAGGTTTGGTGGTTCANAATATACAACTTAATC	2280
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Qy	2521	TGTGAACAGCAATTTATTATTTTGTCTCATCAAAATATAAAGGATTTTTTTTCACTTGAA	2580
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Qy	2581	AAAAAAAAAAAAAAAAAAAAAAAAAAAAA	2609
Db	2581	AAAAAAAAAAAAAAAAAAAAAAAAAAAAA	2609

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RESULT 3
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; Sequence 174, Application US/10157031
; Publication No. US20030108890A1
; GENERAL INFORMATION:
; APPLICANT: Baranova, A. V.
; APPLICANT: Yankovsky, N. K.
; APPLICANT: Kozlov, A. P.
; APPLICANT: Lobashev, A. V.
; APPLICANT: Krukovskaya, L. L.
; TITLE OF INVENTION: In silico screening for phenotype-associated expressed s
; FILE REFERENCE: 2760-1C3
; CURRENT APPLICATION NUMBER: US/10/157,031
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 415
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 174
; LENGTH: 2609
; TYPE: DNA
; ORGANISM: Homo sapiens
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; NAME/KEY: misc feature
; LOCATION: (2025)..(2025)
; OTHER INFORMATION: n = unknown
; FEATURE:
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; LOCATION: (2036)..(2036)
; OTHER INFORMATION: n = unknown
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2164)..(2164)
; OTHER INFORMATION: n = unknown
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2264)..(2264)
; OTHER INFORMATION: n = unknown
US-10-157-031-174

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RESULT 4
 US-10-318-906A-1
 ; Sequence 1, Application US/10318906A
 ; Publication No. US20030157678A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lambeth, J. David
 ; APPLICANT: Griending, Kathy
 ; APPLICANT: Lassegue, Bernard
 ; APPLICANT: Arnold, Rebecca S.
 ; APPLICANT: Cheng, Guangjie
 ; TITLE OF INVENTION: Mitogenic Oxygenases
 ; FILE REFERENCE: 05501-0221
 ; CURRENT APPLICATION NUMBER: US/10/318,906A
 ; CURRENT FILING DATE: 2002-12-13
 ; PRIOR APPLICATION NUMBER: US 09/437,568
 ; PRIOR FILING DATE: 1999-11-10
 ; NUMBER OF SEQ ID NOS: 61
 ; SOFTWARE: Patent In Ver. 2.0
 ; SEQ ID NO 1
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 ; FEATURE:
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RESULT 6
US-10-393-590-13
; Sequence 13, Application US/10393590
; Publication No. US20030190656A1
; GENERAL INFORMATION:
; APPLICANT: WANG, YIXIN
; TITLE OF INVENTION: BREAST CANCER PROGNOSTIC PORTFOLIO
; FILE REFERENCE: CDS 268 US NP
; CURRENT APPLICATION NUMBER: US/10/393,590
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/368,789
; PRIOR FILING DATE: 2002-03-29
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 2609
; TYPE: DNA
; ORGANISM: human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2025)..(2025)
; OTHER INFORMATION: any kind of base
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2036)..(2036)
; OTHER INFORMATION: any kind of base
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2164)..(2164)
; OTHER INFORMATION: any kind of base
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2264)..(2264)
; OTHER INFORMATION: any kind of base
US-10-393-590-13

Query Match 99.8%; Score 2605; DB 15; Length 2609;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2609; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGATAGCACAGTTCTGTCCAGAGAAAGGAGCGGAATAAACTTTATTCATTTCCAGGAA 60
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Db 61 CTCCTGGGTAGTGTGTGTTTTCATCTTTAAAGGCTCACAGACCTCGCGCTGGACAA 120
QY 121 ATGTTCCATTCTGAGGACCTCTCAGAAATCGGAATGCTGAAATCTTCCCTGTTGCCTA 180
Db 121 ATGTTCCATTCTGAGGACCTCTCAGAAATCGGAATGCTGAAATCTTCCCTGTTGCCTA 180
QY 181 GAAGGCTCCAAACCACTCTTGACAAATGGGAACTGGGTGTTAACCACTGGTTTCAG 240
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QY 241 TTTTGTCTGTGTTGTTTGGTTAGGGCTGAATGTTTCCCTGTTGTTGAGTGCCTTCCTGA 300
Db 241 TTTTGTCTGTGTTGTTTGGTTAGGGCTGAATGTTTCCCTGTTGTTGAGTGCCTTCCTGA 300
QY 301 AATATGAGAGGCGGCAAAATACTACTACAAAGAAAAATCCTTGGGTCAACATGCGCT 360
Db 301 AATATGAGAGGCGGCAAAATACTACTACAAAGAAAAATCCTTGGGTCAACATGCGCT 360
QY 361 GTGCCGAGGCTGTGCTCTCTGCTTGAATTTTAAACAGACGCTGATCCTGCTCCTGT 420
Db 361 GTGCCGAGGCTGTGCTCTCTGCTTGAATTTTAAACAGACGCTGATCCTGCTCCTGT 420
QY 421 GTCCCAATCTGCTGCTTCTCGAGGGGACCTGCTCATTTTCAGCCGCACTGAGAA 480
Db 421 GTCCCAATCTGCTGCTTCTCGAGGGGACCTGCTCATTTTCAGCCGCACTGAGAA 480
QY 481 AGCAATTGGATCAAACTCTACCTTCCAAAGCTGGTGGCTATATGATCTGCTACATA 540
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QY 541 CAGCTATTACATCATTTGACACCTGTTTAACTTTGACTGCTATAGCAGAGCGCAGG 600
Db 541 CAGCTATTACATCATTTGACACCTGTTTAACTTTGACTGCTATAGCAGAGCGCAGG 600
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Db 661 GTTCTTGGCTAAATCCATCCAGTCCCGAAACACAGACAGTGGAGTATGACATTCACCA 720
QY 721 GGTGCTGCTGCTCATCTGAGTATCATGACAAATAGCCTTGAATCTCATGTTCACTTCAG 780
Db 721 GGTGCTGCTGCTCATCTGAGTATCATGACAAATAGCCTTGAATCTCATGTTCACTTCAG 780
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Db 781 CTACTGAGTTCACTCCGAGGAGTTATTTTGAAGTCTTCTGGTATATCTCACCACCTTTTA 840
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Db 841 TCTTCTATATCTTGGCTTAGGATTCACGGCATTTGGTGAATGTCGGGGTCAAAACAG 900
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QY 1021 GGATCTTGACCGGTCACTTTTATATCTGTAAGAGTATCTCCGGTTTATACCGCTCC 1080
Db 1021 GGATCTTGACCGGTCACTTTTATATCTGTAAGAGTATCTCCGGTTTATACCGCTCC 1080
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Db 1201 TCTCTCTCTGGAATGGCATCTTTTACTTTGACCTCTGCTCCAGAGGAATTTCTTCT 1260
QY 1261 CCATTCATATCCGAGCAGAGGGGAGCTGACAGAAAAATCTCATAGGGCTTTTCGAACAC 1320
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Db 1261 CCATTCTATCCGAGCAGGAGGACTGGACAGAAATCTCATAGGGCTTTTCGARCAAC 1320
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 Db 1381 TTTTCCAGTATGAAGTGGCTGTGCTGTGGAGCAGGAATTTGGGTCAACCCCTTTGCTT 1440
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 Db 1621 TCTTCCCTCAGCGATGGACAGCAATTTGTTGTCATGCGACATTAACCTTGACAAAG 1680
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 Db 1681 CCACTGACATCGTGACAGGTCTGAAAACAGAAAACTCTCTTGGAGACCAATTTGGGACA 1740
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 Db 1741 ATGAGTTTTCTACAAATAGTACCTCCACCCCAAGTCTGTAGTGGAGTTTTCTTATGTG 1800
 Qy 1801 GCCCTCGGACTTTGGCAAGAGCCTGGCAATCTGTCAACCGATATTCAGTCTGGATC 1860
 Db 1801 GCCCTCGGACTTTGGCAAGAGCCTGGCAATCTGTCAACCGATATTCAGTCTGGATC 1860
 Qy 1861 CTAGAAAGGTTCAATCTCTTGTATCTTCAAGAAATTTTGGATTTAGGATTAAGGACGG 1920
 Db 1861 CTAGAAAGGTTCAATCTCTTGTATCTTCAAGAAATTTTGGATTTAGGATTAAGGACGG 1920
 Qy 1921 TAATCTGATTTGCTCTTTGTATCTTCAAGAAATTTTGGATTTAGGATTAAGGACGGTAA 1980
 Db 1921 TAATCTGATTTGCTCTTTGTATCTTCAAGAAATTTTGGATTTAGGATTAAGGACGGTAA 1980
 Qy 1981 TCTGATTTTGTCTCTTTGTATCTTCAAGAAATTTTGGATTTAGGATTTAGGACGGTAA 2040
 Db 1981 TCTGATTTTGTCTCTTTGTATCTTCAAGAAATTTTGGATTTAGGATTTAGGACGGTAA 2040
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 Db 2101 CATTCAACTCTGTTTACTTGTAGCTTCAAGAAATTTTGGATTTAGGATTTAGGACGGTAA 2160
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 Db 2161 GAANTTTCTAAAGCCCATGGATCTTCTCAGAAAAATAAAGTAAATCTTTCTGGACAG 2220
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 Db 2221 CCATGACTGTAGCAGGCTTGTATGACAGAAATTTGGTGTTCANAAATTAACAATAATC 2280
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 Qy 2341 TCCCTCCCAACCCCAAGATTTTAAAGTGGGTGACTTTTTTAAATAAAAAATTTATTTGA 2400
 Db 2341 TCCCTCCCAACCCCAAGATTTTAAAGTGGGTGACTTTTTTAAATAAAAAATTTATTTGA 2400

Qy 2401 ATAAATTAATCAATAAACAATAAATAAACAATAAATAAACAATAAATAAACAATAAATAA 2460
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 Qy 2521 TGTGAACAGCAATTTATTTATTTTGTCTCATCAAAAAATAAAGGATTTTTTTCACCTTGA 2580
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 Qy 2581 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2609
 Db 2581 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2609

RESULT 7
 US-10-393-567-13
 ; Sequence 13, Application US/10393567
 ; Publication No. US20030194733A1
 ; GENERAL INFORMATION:
 ; APPLICANT: WANG, YIXIN
 ; TITLE OF INVENTION: CANCER DIAGNOSTIC PANEL
 ; FILE REFERENCE: CDS 269 US NP
 ; CURRENT APPLICATION NUMBER: US/10/393,567
 ; CURRENT FILING DATE: 2003-03-21
 ; PRIOR APPLICATION NUMBER: 60/368,667
 ; PRIOR FILING DATE: 2002-03-29
 ; NUMBER OF SEQ ID NOS: 100
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 13
 ; LENGTH: 2609
 ; TYPE: DNA
 ; ORGANISM: human
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (2025)..(2025)
 ; OTHER INFORMATION: any kind of base
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (2036)..(2036)
 ; OTHER INFORMATION: any kind of base
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (2164)..(2164)
 ; OTHER INFORMATION: any kind of base
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 ; NAME/KEY: misc feature
 ; LOCATION: (2264)..(2264)
 ; OTHER INFORMATION: any kind of base
 ; US-10-393-567-13

Query Match 99.8%; Score 2605; DB 15; Length 2609;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2609; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTGATAGCAGAGTTCTGTCTCAGAGAGGAGGCGGAATAAATTTATTTATTTCCAGGAA 60
 Db 1 GCTGATAGCAGAGTTCTGTCTCAGAGAGGAGGCGGAATAAATTTATTTATTTCCAGGAA 60
 Qy 61 CTCCTGGGTAGGTGTGTTTTTTCACATCTTAAAGGCTCAGACCTCGCTCGACAA 120
 Db 61 CTCCTGGGTAGGTGTGTTTTTTCACATCTTAAAGGCTCAGACCTCGCTCGACAA 120
 Qy 121 ATGTTCCATCTCTGAAGACCTCTCCAGAAATCCGGAATTCGGAATCTTCCCTGTTGCCTA 180
 Db 121 ATGTTCCATCTCTGAAGACCTCTCCAGAAATCCGGAATTCGGAATCTTCCCTGTTGCCTA 180
 Qy 181 GAAGGCTCCAAACACCACTCTTGAATGGGAACTGGTGTAAACCACTGGTTTTCAG 240
 Db 181 GAAGGCTCCAAACACCACTCTTGAATGGGAACTGGTGTAAACCACTGGTTTTCAG 240

QY	241	TTTTGCTTTCTGCTGTGTTGGTTAGGCGTGAATGTTTTCTGTTTCTGTTTCTGTTGAGTGGCTTCTCTCGA	300
DB	241	TTTTTGTTTCTGTTCTGTTTGGTTAGGCGTGAATGTTTTCTGTTTCTGTTTCTGTTTCTGTTGAGTGGCTTCTCTCGA	300
QY	301	AATATGAGAAGCCCGACAAAATACTACTACACAAGAAAAATCCTTGGGTCAACATTTGGCCT	360
DB	301	AATATGAGAAGCCCGACAAAATACTACTACACAAGAAAAATCCTTGGGTCAACATTTGGCCT	360
QY	361	GTGCCGAGCGTCTGCTCTCTGCTTTGAATTTTAAACAGACGCTGATCTGCTTCTGTTCTGTGT	420
DB	361	GTGCCGAGCGTCTGCTCTCTGCTTTGAATTTTAAACAGACGCTGATCTGCTTCTGTTCTGTGT	420
QY	421	GTGCAATCTGCTGTCTCTTCTGAGGGGCACCTGCTCATTTTTCAGACGCGCACACTGAGAA	480
DB	421	GTGCAATCTGCTGTCTCTTCTGAGGGGCACCTGCTCATTTTTCAGACGCGCACACTGAGAA	480
QY	481	AGCAATTTGGATCACAACTCTACCTTTCCACAAGCTGGTGGCCTATATGATCTGCCTACATA	540
DB	481	AGCAATTTGGATCACAACTCTACCTTTCCACAAGCTGGTGGCCTATATGATCTGCCTACATA	540
QY	541	CAGCTTATTCACATCATTCGACACCTGTTTAACTTTGACTGTGTAGCAGAAACGACACAG	600
DB	541	CAGCTTATTCACATCATTCGACACCTGTTTAACTTTGACTGTGTGTAGCAGAAACGACACAG	600
QY	601	CCACAGATGGCTCCCTTGCCTCCATCTCTCCAGCCTATCTCATGATCAGAAAAAGGGGG	660
DB	601	CCACAGATGGCTCCCTTGCCTCCATCTCTCCAGCCTATCTCATGATCAGAAAAAGGGGG	660
QY	661	GTTCTTGGCTAAATCCCATCCAGTCCCGAAACAGACAGTGGAGTATGTGACATTCACCA	720
DB	661	GTTCTTGGCTAAATCCCATCCAGTCCCGAAACAGACAGTGGAGTATGTGACATTCACCA	720
QY	721	GCCTTGTGCTCAGCTGGAGTGATCATGACAATAGCCTTGATTTCTCATGTGTAACTTCAG	780
DB	721	GCCTTGTGCTCAGCTGGAGTGATCATGACAATAGCCTTGATTTCTCATGTGTAACTTCAG	780
QY	781	CTACTGAGTTTCATCCGGAGGAGTTATTTTGAAGTCTTCTGCTGTATCTACCAACCTTTTTA	840
DB	781	CTACTGAGTTTCATCCGGAGGAGTTATTTTGAAGTCTTCTGCTGTATCTACCAACCTTTTTA	840
QY	841	TCTTCTATATCTTTGGCTTAGGGATTCACGGCATTTGGTGAATTTGTCGGGGTCAAAACAG	900
DB	841	TCTTCTATATCTTTGGCTTAGGGATTCACGGCATTTGGTGAATTTGTCGGGGTCAAAACAG	900
QY	901	AGGAGACATGAATGAGAGTTCATCCTCGCAAGTGTGCAGAGTCTTTTTCAGATGTGGGATG	960
DB	901	AGGAGACATGAATGAGAGTTCATCCTCGCAAGTGTGCAGAGTCTTTTTCAGATGTGGGATG	960
QY	961	ATCGTGACTCCCATCTGTAGGCGCCCTTAAGTTTGAAGGCGCATCCCGCTGAGTCTTTGGAAGT	1020
DB	961	ATCGTGACTCCCATCTGTAGGCGCCCTTAAGTTTGAAGGCGCATCCCGCTGAGTCTTTGGAAGT	1020
QY	1021	GGATCTTTGCAACGGTCAATCTTTTATATCTGTGAAAGGATCTCTCCGGTTTTCACCGCTCCC	1080
DB	1021	GGATCTTTGCAACGGTCAATCTTTTATATCTGTGAAAGGATCTCTCCGGTTTTCACCGCTCCC	1080
QY	1081	AGCAGAGGTTGTATTCACCAAGTGTGTATGCACCCATCCAAAGTTTTTGGAAATTCGAGA	1140
DB	1081	AGCAGAGGTTGTATTCACCAAGTGTGTATGCACCCATCCAAAGTTTTTGGAAATTCGAGA	1140
QY	1141	TGAACAAGCGTGGCTTCAGCATGGAAGTGGGGCAGTATATCTTTTGTAAATGCGCCCTCAA	1200
DB	1141	TGAACAAGCGTGGCTTCAGCATGGAAGTGGGGCAGTATATCTTTTGTAAATGCGCCCTCAA	1200
QY	1201	TCTCTCTCTGGAATGGCATCTTTTACTTTTACTTTTACTTTGACCTCTGCTCCAGAGGAATTTCTTCT	1260
DB	1201	TCTCTCTCTGGAATGGCATCTTTTACTTTTACTTTTACTTTTACTTTTACTTTTACTTTCT	1260
QY	1261	CCATTCTATATCCGAGCAGCGGGACCTGGACAGAAAATCTCATAGGGCTTTCGAAACAC	1320
DB	1261	CCATTCTATATCCGAGCAGCGGGACCTGGACAGAAAATCTCATAGGGCTTTCGAAACAC	1320

QY	1321	AAATATCCACAAATCCAGATTTGAGTTGAGTGGTCCCTTTGGCACACGCCAGTGAAGGATG	1380
DB	1321	AAATATCCACAAATCCAGGATTTGAGTTGAGTGGTCCCTTTGGCACACGCCAGTGAAGGATG	1380
QY	1381	TTTTCCAGTATGAAGTGGCTGTGCTGTGGAGCAGGAATTTGGGTGACCCCTTTGGCTT	1440
DB	1381	TTTTCCAGTATGAAGTGGCTGTGCTGTGGAGCAGGAATTTGGGTGACCCCTTTGGCTT	1440
QY	1441	CTATCTTGAATCCATCTGGTCAAAATTCAGTGTGCAGACCAACAACCTCAAAACAAAA	1500
DB	1441	CTATCTTGAATCCATCTGGTCAAAATTCAGTGTGCAGACCAACAACCTCAAAACAAAA	1500
QY	1501	AGATCTATTTCTACTGGATCTGCAGGGAGACAGGTGCTTTTCTGGTTCACAAACCTGT	1560
DB	1501	AGATCTATTTCTACTGGATCTGCAGGGAGACAGGTGCTTTTCTGGTTCACAAACCTGT	1560
QY	1561	TGACTTTCCCTGGAAACAGGAGATGGAGAAATTAGGCAAGTGGTTTTCTAACTACCGTC	1620
DB	1561	TGACTTTCCCTGGAAACAGGAGATGGAGAAATTAGGCAAGTGGTTTTCTAACTACCGTC	1620
QY	1621	TCTTCCTCACCGGATGGGACAGCAATATTTGTGGTCAATCAGACATTAACCTTGACAAGG	1680
DB	1621	TCTTCCTCACCGGATGGGACAGCAATATTTGTGGTCAATCAGACATTAACCTTGACAAGG	1680
QY	1681	CGACTGACATCTGTGACAGGTCTGAAACAGAAAAACCTCCTTTGGGAGACCAATGTGGGACA	1740
DB	1681	CGACTGACATCTGTGACAGGTCTGAAACAGAAAAACCTCCTTTGGGAGACCAATGTGGGACA	1740
QY	1741	ATGAGTTTTTCTACAATAGCTACCTCCACCCCAAGTCTGTAGTGGGAGTTTTCTTATGTG	1800
DB	1741	ATGAGTTTTTCTACAATAGCTACCTCCACCCCAAGTCTGTAGTGGGAGTTTTCTTATGTG	1800
QY	1801	GGCCTCGGACTTTGGCAAAAGAGCCTCGCAAAATGCTGTCAACCATATTTCCAGTCTGGATC	1860
DB	1801	GGCCTCGGACTTTGGCAAAAGAGCCTCGCAAAATGCTGTCAACCATATTTCCAGTCTGGATC	1860
QY	1861	CTAGAAAGGTTCAAATTTCTACTTCAACAAAGAAAAATTTTTCAGTTATAGGAATAGGACGG	1920
DB	1861	CTAGAAAGGTTCAAATTTCTACTTCAACAAAGAAAAATTTTTCAGTTATAGGAATAGGACGG	1920
QY	1921	TAATCTGCATTTTGTCTCTTTGTATCTTCAGTAAATTTAGGAAATAGGACGGTAA	1980
DB	1921	TAATCTGCATTTTGTCTCTTTGTATCTTCAGTAAATTTAGGAAATAGGACGGTAA	1980
QY	1981	TCTGCATTTTGTCTCTTTGTATCTTCAGTAAATTTAGTGTCTCNTCAGGTTTGACNAGT	2040
DB	1981	TCTGCATTTTGTCTCTTTGTATCTTCAGTAAATTTAGTGTCTCNTCAGGTTTGACNAGT	2040
QY	2041	GACTTTAGGATTAAGAAATGTCCTCTCAAGCCTTGACTCCCTGGTATTTCTTTTGTGATG	2100
DB	2041	GACTTTAGGATTAAGAAATGTCCTCTCAAGCCTTGACTCCCTGGTATTTCTTTTGTGATG	2100
QY	2101	CAATCAACTTCCTTACTTTCAGCTTCAGCAACTTTAAGAACTTTCTTGAAGTTCT	2160
DB	2101	CAATCAACTTCCTTACTTTCAGCTTCAGCAACTTTAAGAACTTTCTTGAAGTTCT	2160
QY	2161	GAAATTTCTTAAAGCCCATGGATCCTTCTCAGAAAAATAACTGTAATCTTTCTCGGACAG	2220
DB	2161	GAAATTTCTTAAAGCCCATGGATCCTTCTCAGAAAAATAACTGTAATCTTTCTCGGACAG	2220
QY	2221	CCATGACTGTAGCAGGCTTGATAGCAGAAAGTTTGGTGGTTCCANAATTAACAACCTAAATC	2280
DB	2221	CCATGACTGTAGCAGGCTTGATAGCAGAAAGTTTGGTGGTTCCANAATTAACAACCTAAATC	2280
QY	2281	CCAGTGATTTTATCAATTCAGTGTACCATCTCCTGAGTTTTGGTTGTGTAATCTTTTG	2340
DB	2281	CCAGTGATTTTATCAATTCAGTGTACCATCTCCTGAGTTTTGGTTGTGTAATCTTTTG	2340
QY	2341	TCCCTCCCAACCCCAAGAAATTTTAAAGTGGGTGACTTTTAAATAAAAAATTTATGTA	2400
DB	2341	TCCCTCCCAACCCCAAGAAATTTTAAAGTGGGTGACTTTTAAATAAAAAATTTATGTA	2400
QY	2401	ATAATTAATGATAAAACATAATAATAATAATAATAAAACAAATTAACCGGAACCC	2460


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QY 1261 CCATTCATATCCGAGCAGCAGGGGACTGGACAGAAAATCTCATAGGGCTTTTGAACAAC 1320
Db 1261 CCATTCATATCCGAGCAGCAGGGGACTGGACAGAAAATCTCATAGGGCTTTTGAACAAC 1320
QY 1321 AATATTACCAAATCCCAAGATTTGAAGTGGATGGTCCCTTTGGCAGACAGCCAGTGAGGATG 1380
Db 1321 AATATTACCAAATCCCAAGATTTGAAGTGGATGGTCCCTTTGGCAGACAGCCAGTGAGGATG 1380
QY 1381 TTTTCCAGTANGAAGTGGCTGTCTGGTTGGAGCAGGAATTTGGGGTCAACCCCTTTGCTT 1440
Db 1381 TTTTCCAGTANGAAGTGGCTGTCTGGTTGGAGCAGGAATTTGGGGTCAACCCCTTTGCTT 1440
QY 1441 CTATCTTGGAATCAATCTGGTACAAATTCAGTGTGAGACCAACACCTCAAAAACAAAA 1500
Db 1441 CTATCTTGGAATCCATCTGGTACAAATTCAGTGTGAGACCAACACCTCAAAAACAAAA 1500
QY 1501 AGATCTATTCTTACTGGATCTGCAGGGAGACAGGTGCTTTTCTCGTTTCAACAACCTGT 1560
Db 1501 AGATCTATTCTTACTGGATCTGCAGGGAGACAGGTGCTTTTCTCGTTTCAACAACCTGT 1560
QY 1561 TGACTTCCCTGGAAACAGGAGATGGAGGAATTAGGCCAAAGTGGTTCCTAAATCTACCGTC 1620
Db 1561 TGACTTCCCTGGAAACAGGAGATGGAGGAATTAGGCCAAAGTGGTTCCTAAATCTACCGTC 1620
QY 1621 TCTTCTCTCACCGGATGGGACAGCAATATTTGGTTCATGACAGCAATTAACCTTTGACAAG 1680
Db 1621 TCTTCTCTCACCGGATGGGACAGCAATATTTGGTTCATGACAGCAATTAACCTTTGACAAG 1680
QY 1681 CCACTGACATCGTGACAGTCTGAAAACAGAAAACCTCCTTTGGGAGACCAATGTGGGACA 1740
Db 1681 CCACTGACATCGTGACAGTCTGAAAACAGAAAACCTCCTTTGGGAGACCAATGTGGGACA 1740
QY 1741 ATGAGTTTTCTCAATAGTACTCTCCACCCCAAGTCTGTAGTGGAGTTTTCTTATGTG 1800
Db 1741 ATGAGTTTTCTCAATAGTACTCTCCACCCCAAGTCTGTAGTGGAGTTTTCTTATGTG 1800
QY 1801 GGCCTCGACTTTGGCAAGAGCTCGCAAAATGCTGTACCGATATTCAGTCTGGATC 1860
Db 1801 GGCCTCGACTTTGGCAAGAGCTCGCAAAATGCTGTACCGATATTCAGTCTGGATC 1860
QY 1861 CTAGAAAGGTTCAATCTACTCTTCAACAAAGAAAATTTTGGTTATAGGAATAAGGACGG 1920
Db 1861 CTAGAAAGGTTCAATCTACTCTTCAACAAAGAAAATTTTGGTTATAGGAATAAGGACGG 1920
QY 1921 TAACTCGCAATTTGTCTCTTTGTATCTTCAGTAATGAGTTATAGGAATAAGGACGGTAA 1980
Db 1921 TAACTCGCAATTTGTCTCTTTGTATCTTCAGTAATGAGTTATAGGAATAAGGACGGTAA 1980
QY 1981 TCTGCATTTTGTCTCTTGTATCTTCAAGTAATTTACTTGGTCTCNTCAGTTTGANCAGT 2040
Db 1981 TCTGCATTTTGTCTCTTGTATCTTCAAGTAATTTACTTGGTCTCNTCAGTTTGANCAGT 2040
QY 2041 CACTTTAGGATAAGATGTGCCTCTCAAGCCTTGACTCCCTGGTATTCCTTTTTTGTATG 2100
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QY 2101 CATTCAACTTCGTTACTTGAGCTTCAGCAACTTAAGAACTTCTGAAGTCTTAAAGTTCT 2160
Db 2101 CATTCAACTTCGTTACTTGAGCTTCAGCAACTTAAGAACTTCTGAAGTCTTAAAGTTCT 2160
QY 2161 GAANTTCTTAAAGCCCATGATCCTTCTCAGAAAATAACTGTAAATCTTCTGGACAG 2220
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QY 2281 CCAGGTGATTTTATCAATTCAGTGTACCATCTCTCTGAGTTTGGTTTGTAAATCTTTTG 2340
Db 2281 CCAGGTGATTTTATCAATTCAGTGTACCATCTCTCTGAGTTTGGTTTGTAAATCTTTTG 2340
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QY 2341 TCCTCTCCACCCCCCAACAGAGATTTTAAGTAGGTGACTTTTAAATAAAAAATTTATTGA 2400
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QY 2401 ATAATTAATGATAAACAATAATAAACAATAATAAACAATAAACAATAAACAATAAACA 2460
Db 2401 ATAATTAATGATAAACAATAATAAACAATAATAAACAATAAACAATAAACAATAAACA 2460
QY 2461 ATCCCATATAACACCAACAGTGATACATGTTTACTGTCACCTTTTGATATGTTTATCCAG 2520
Db 2461 ATCCCATATAACACCAACAGTGATACATGTTTACTGTCACCTTTTGATATGTTTATCCAG 2520
QY 2521 TGTGAACAGCAATTTATTTTGTCTCATCAAAAAATAAAGGATTTTTTTCACCTGAA 2580
Db 2521 TGTGAACAGCAATTTATTTTGTCTCATCAAAAAATAAAGGATTTTTTTCACCTGAA 2580
QY 2581 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2609
Db 2581 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2609
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RESULT 9

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US-10-318-906A-22
; Sequence 22, Application US/10318906A
; Publication No. US20030157678A1
; GENERAL INFORMATION:
; APPLICANT: Lambeth, J. David
; APPLICANT: Griendling, Kathy
; APPLICANT: Lasseque, Bernard
; APPLICANT: Arnold, Rebecca S.
; APPLICANT: Cheng, Guangjie
; TITLE OF INVENTION: Mitogenic Oxygenases
; FILE REFERENCE: 05501-0221
; CURRENT APPLICATION NUMBER: US/10/318,906A
; PRIOR FILING DATE: 2002-12-13
; PRIOR APPLICATION NUMBER: US 09/437,568
; PRIOR FILING DATE: 1999-11-10
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 2577
; TYPE: DNA
; ORGANISM: Rat
US-10-318-906A-22
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Query Match 50.0%; Score 1305; DB 15; Length 2577;
Best Local Similarity 83.4%; Pred. No. 0;
Matches 1495; Conservative 0; Mismatches 295; Indels 3; Gaps 1;
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QY 132 CTGAAGGACCTCTCCAGAAATCCGGATTGCTGAATCTTCCCTGTGCTAGAAAGGGCTCCA 191
Db 53 CAGAAAGTTCCTATCCTGAAGGATCCCATCAGAGAAACAGATTGCTCTAAAGGGCTCCA 112
QY 192 AACCACTCTTGACAAATGGGAACTGGGTGGTTAACCACTGGTTTCACTGTTTGTCTG 251
Db 113 GACCTCCCAATTTGACAAATGGGAACTGGGTGGTTAACCACTGGCTCTCAGTTTGTCTG 172
QY 252 GTTGTGTTGGTAGGCTGAAATGTTTTTCTGTTTGGATGCCCTTCTGAAATATGAGAG 311
Db 173 GTTCTTGGTGGGCTGAAACATTTTCTGTTTGTAGCTTCTCTGAATATGAGAG 232
QY 312 GCCGCAAAATACTACTACACAAGAAAAATCCCTGGGTCAACATTTGGCTGTGCCGAGCG 371
Db 233 TCTGACAAAGTACTATTAACAGAGAGAAATCTCGGAACTGCTTGGCTTGGCCAGACA 292
QY 372 TCTGCTCTCTGCTTGAATTTTAAACGACCGTGTATCTCTGCTTCTGTGTGCGCAATCTG 431
Db 293 TCTGCTTTGTGCTGAAATTTTAAACAGCATGTGTATCTCTGATTCCTGTGTGCGAAATCTG 352
QY 432 CTGCTCTTCTGAGGGGACCTGCTCATTTTGCAGCCGACACACTGAGAAAGCAATTTGAT 491
Db 353 CTCCTCTTCTGAGGGGACCTGTCTCATTTTGCACCAACACACGCTGAGAAAGCCATTTGAT 412
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Qy	492	CACAACCTCACCTTCCAAAGCTGGTGGCCATATATGATCTGCCTACATACAGCTAATTCAC	551
Db	413	CACAACCTCACCTTCCATAAGCTGGTGGCATAATATGATCTGCATAATTCACAGCTAATTCAT	472
Qy	552	ATCATTCGCACACCTGTTTAACTTTTGACTGCTATAGCAGAAGCCGACAGGCCACAGATGCG	611
Db	473	ATCATTCGCACATCTATTTTAACTTTTGAACGCTACAGTAGAAGCCAAACAGGCCATGGAATGA	532
Qy	612	TCCCTTGCTCCTCAATCTCTCCAGCCTATCTCATGATGAGAAAAAGGGGGTCTCTGGCTTA	671
Db	533	TCTCTTGCTCTGTCTCTCCAGCCATTCATCCCGAGAAA--GAAGATCTTGGCTTA	589
Qy	672	AATCCCATCCAGTCCCGAAAAACAACAGAGTGGAGTATGTGACATTCACCAAGCGTTGCTGGT	731
Db	590	AATCCCATCCAGTCTCCAAACGTGACAGTGATGTATGCAGCAATTTACCAGTATGCTGGC	649
Qy	732	CTGACTGGAGTGATCATGACAAATAGCCTTGATTTCTCATGTACTATCTCAGCTACTGAGTTC	791
Db	650	CTTACTCGAGTGGTGGCCACTGTGGCTTTGGTTCTCATGTGTAATCTCAGCTATGGAAGTTT	709
Qy	792	ATCCGGAGGAGCTTATTTTGAAGTCTTCTGGTATACTCACCACCTTTTATATCTTCTATATC	851
Db	710	ATCCGCAAGGAATTAATTTTGAGCTCTTCTGGTATACATCATCCCTTTTCATCATCTATATC	769
Qy	852	CTTGGCTTTAGGGAATTCACGGCAATGGTGGAAATGTCCGGGGTCAACACAGAGGAGACATG	911
Db	770	ATCTGCTTTAGGATCCATGGCTCGGGGGGATGTCCGGGGTCAACACAGAAGAGAGCATG	829
Qy	912	AATCAGAGTCACTCTCGCAAGTGTGCAGAGTCTTTTGAGATGTGGGATGATCGTACTCC	971
Db	830	AGTGAAGAGTCATCCCGCAACTGTTTCATCTCTTTCCACGAGTGGGATAAGTATGAAGG	889
Qy	972	CACGTAGCGGCCCTAAGTTTGAAGGGCATCCCCCTCAGTCTTGGGAAGTGGATCTTGCA	1031
Db	890	AGTTGCAGAGTCTCTCATTTTGTGGGGCAACCCCTGAGTCTTGGAAAGTGATCTCGCG	949
Qy	1032	CCGGTCAATCTTTATATCTGTGAAGGATCCTCCGGTTTATCCGCTCCCAAGCAGAAAGTT	1091
Db	950	CCGATTGCTTTTATATCTTTGAAGGATCCTTCGCTTTTATCGTCCCGCAGAAAGTTC	1009
Qy	1092	GTGATTACCAAGGTTGTTATGCACCCATCCAAAGTTTGGAAATGCGAGATGAACAAGCGT	1151
Db	1010	GTGATTACCAAGGTTGTCAATGCACCCCATGTAAAGTTTGGAAATGTCAGATGAGGAAGCGG	1069
Qy	1152	GGCTTTCAGCATGGAAGTGGGCGAGTATATCTTGTAAATTCGCCCTCAATCTCTCTCCTG	1211
Db	1070	GGCTTTACTATGGGAATAGGAACAGTATATTCGTAATTCGCCCTCGATTTCTCTCCTG	1129
Qy	1212	GAATGGCAATCCTTTTACTTTTGACCTCTGCTCCAGAGGAAGATTTCTTCTCCATTCATATC	1271
Db	1130	GAATGGCATCCCTTTACTCTGACCTCTGCTCCAGAGGAAGAAATTTTCTCCATTCATATT	1189
Qy	1272	CGAGCAGCAGGGGACTGGACAGAAAACTCATAGAGGTTTTCGAAACAACAAATATTACCA	1331
Db	1190	CGAGCAGCAGGGGACTGGACAGAAAACTCATAGAGGAATTTGGAACAACACAGCACTCACCA	1249
Qy	1332	ATTTCACGAGTGAAGTGGATGGTCCCTTGGCACAGCCAGTGAAGGATGTTTCCAGTAT	1391
Db	1250	ATGCCCAGGATCGAGTGGATGGTCCCTTTGGCACAGTCACTGAGGAGTGTCTCCAGTAC	1309
Qy	1392	GAAGTGGTGTGCTGGTTGGACAGGAATGGGGTGCACCCCTTTGCTTCTATCTTGAAA	1451
Db	1310	GAAGTGGCTGTACTGGTTGGGGCAGGGATGCGCTCACTCCCTTTGCTTCTTCTTGAAA	1369
Qy	1452	TCCATCTGGTCAAAATTCAGTGTGCAGACCAACCTCAAAAACAAAAAGATCTATTTTC	1511
Db	1370	TCATCTGGTCAAAATTCAGCGTGCACACAACAAGCTGAAAAACAAAAAGATCTATTTTC	1429
Qy	1512	TACTGGATCTGCAGGAGACAGGTGCCCTTTTCTGGTTCACACCACTGTGTGACTTCCCTG	1571
Db	1430	TACTGGATTTGTAGAGACAGCGGTGCCCTTTGCTGGTTCACAACACTATTTGAATTCCTG	1489
Qy	1572	GAACAGGAGATGGAGGAATTAGCCAAAGTGGGTTTCTTAAACTACCGTCTCTTCTCCTCAC	1631

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RESULT 10
US-10-319-236A-22
; Sequence 22, Application US/10319236A
; Publication NO. US20030166198A1
; GENERAL INFORMATION:
; APPLICANT: Lambeth, J. David
; APPLICANT: Griendling, Kathy
; APPLICANT: Lassegue, Bernard
; APPLICANT: Arnold, Rebecca S.
; APPLICANT: Cheng, Guangjie
; TITLE OF INVENTION: Antibodies to Mitogenic Oxygenases
; FILE REFERENCE: 05501-0220 (43150-281176)
; CURRENT APPLICATION NUMBER: US/10/319,236A
; CURRENT FILING DATE: 2002-12-13
; PRIOR APPLICATION NUMBER: US 09/437,568
; PRIOR FILING DATE: 1999-11-10
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 22
; LENGTH: 2577
; TYPE: DNA
; ORGANISM: Rat
US-10-319-236A-22

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Query Match	50.0%	Score 1305;	DB 15;	Length 2577;
Best Local Similarity	83.4%	Pred. No. 0;		
Matches 1495: Conservative	0;	Mismatches 295;	Indels 3;	Gaps 1;

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Db 353 CTCTCTCTCTGAGGGGCACTGCTCANTTTGCAACACACAGCGCTGAGAAAGCCATTGGAT 412
QY 492 CACAACTCACCCTTCCACAAGCTGGTGGCCCTATATGATCTGCTCATACATACAGCTATTTCAC 551
Db 413 CACAACTCACCCTTCCATAAGCTGGTGGCCATATATGATCTGCATATTCACAGCTATTTCAT 472
QY 552 ATCATTTGCACACCTGTTTAACTTTGACTGTCTATAGCAAGGCGGACAGGCCACAGATGGC 611
Db 473 ATCATTTGCACATCTATTAACTTTGAACGCTACAGTAGAAGCCAAACAGGCCATGATGGA 532
QY 612 TCCCTTTGCCCTCCATCTCTCCAGCTATCTCATGATGAGAAABAGGGGGTCTCTGGCTA 671
Db 533 TCTCTTTGCCCTCTGTTCTCTCCAGCTATTCCATCCCGAGAAA--GAAGATTTCTTGCTA 589
QY 672 AATCCCATCCAGTCCCGAAACACGACAGTAGTGGAGTATGTGACATTCACACAGCGTTGCTGGT 731
Db 590 AATCCCATCCAGTCTCCAAACGTTGACAGTGTATGTCAGCAITTTACAGTATTTGCTGGC 649
QY 732 CTCACTGGAGTGATCATGACAATAGCTTGAATTTCTCATGTGAATCTTCAGCTACTGAGTTC 791
Db 650 CTTACTGGAGTGGTCCGCCACTGTGGGCTTTGGTTCTCATGGTAACTTTCAGCTATGAGTTT 709
QY 792 ATCCGGAGGAGTTATTTTGAAGTCTTCTGCTATATCTCACACCTTTTATCTTCTATATC 851
Db 710 ATCCGGAGGAGTTATTTTGAAGTCTTCTGCTATATCTCACACCTTTTATCTTCTATATC 769
QY 852 CTTGGCTTAGGATTCACGGCATTTGGTGAATTTGTCGGGGTCAAAACAGAGAGAGCATG 911
Db 770 ATCTGCTTAGGATTCATGCGCTGGGGGATTTGTCGGGGTCAAAACAGAGAGAGCATG 829
QY 912 AATGAGTTCATCTCGCAAGTGTGACAGTCTTTTGAGATGTGGATGATCGTGACTCC 971
Db 830 AGTGAAGTTCATCTCCCGCACTGTTTCATATCTCTTCCAGAGTGGATGAATGAAGG 889
QY 972 CACTGTAGGCGCCCTAAGTTTGAAGGCGATCCCGCTGAGTCTTTGGAAGTGGATCCTTGA 1031
Db 890 AGTTGAGGAGTCTCATTTTGGGGCAACCCCTGAGTCTTTGGAAGTGGATCCTCGCG 949
QY 1032 CGGTCATTTCTTATATCTGTGAAGGATCCTCGGTTTTTACCGCTCCCGCAGAGAGGTT 1091
Db 950 CGGATTTGCTTTTATATCTTGAAGGATCCTTCGCTTTTATCGCTCCCGCAGAGGTC 1009
QY 1092 GTGATTACCAAGTTGTTATGACCCATCCAAAGTTTTTGAATTTGGAATTCAGATGAACAGGCT 1151
Db 1010 GTGATTACCAAGTTGTCATGACCCATGTAAGTTTTTGAATTTGGAATTCAGATGAAGCGG 1069
QY 1152 GGCCTTCAGCATGGAAGTGGGCGAGTATATCTTTGTTAATTTGCGCCCTCAATCTCTCCCTG 1211
Db 1070 GGCCTTACTATGGGAATAGGACAGTATATATCTGTAATTTGCCCTCGAATTTCTTCCTG 1129
QY 1212 GAATGGATCTTTTACTTTGACCTCTGCTCCAGAGGAAGATTTCTTCTCCATTCATATC 1271
Db 1130 GAATGGATCTTTTACTCTGACCTCTGCTCCAGAGGAAGATTTTCTTCCATTCATAT 1189
QY 1272 CGAGCAGAGGGGACTGGACAGAAATCTATAAGGCTTTTGAAACAAATATTCACCA 1331
Db 1190 CGAGCAGAGGGGACTGGACAGAAATCTATAAGGACATTTTGAACAAACAGCACTCACCA 1249
QY 1332 ATTTCCAGGATTTGAAGTGGATGGTCCCTTTGGCAGAGCCAGTGAGGATGTTTTCCAGTAT 1391
Db 1250 ATGCCCAGGATTCGAGTGGATGGTCCCTTTGGCAGTGTGAGGATGCTTTCCAGTAC 1309
QY 1392 GAAGTGGCTGTGCTGGTGGAGAGGAATTTGGGGTTCACCCCTTTTGTCTTCTATCTTGAA 1451
Db 1310 GAAGTGGCTGTACTGGTTGGGGCAGGGATTTGGCGTCACTCCCTTTGCTTCTTCTTGAA 1369
QY 1452 TCCATCTGGTGAATAATTCAGTGTGACACACACAGCTCAAAACAAAAGATCTATTTC 1511
Db 1370 TCTATCTGGTGAATAATTCAGGCTGTGACACAAAGCTGAAACACAAAAGATCTATTTC 1429
QY 1512 TACTGGATCTGAGGGAGACAGTGGCTTTTCTGGTTCAACAACTGTGTGACTTCCCTG 1571
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Db 1430 TACTGGATTTGTAGAGAGAGCGGTGGCTTTTGCCTGGTTCAACAACATTATTGAATTCCTG 1489
QY 1572 GAACAGAGATGAGGAAATTTAGGCAAAAGTGGGTTTTCTAAACTACCGTCTCTTCTCTCAC 1631
Db 1490 GAACAAGATGAGCAAGATTTAGGCAAAACCGGATTTCTAAACTACCGACTCTTCTCTCA 1549
QY 1632 GGATGGGACAGCAATATTTGTTGGTCATGAGCAATTAACCTTTTGAAGGCCACTGACATC 1691
Db 1550 GGCTGGGATAGCAACATTTGCTGTCATGAGCAATTAACCTTTTGAAGGCCACTGAGGTC 1609
QY 1692 GTGACAGGCTTGAACAGAAACCTCTCTTTGGGAGACCAATGTGGGACCAATGATGTTTCT 1751
Db 1610 CTGACAGGCTTGAACAGAAACCTCTCTTTGGGAGACCAATGTGGGACCAATGATGTTTCT 1669
QY 1752 ACAATAGCTACCTCCACCCCAAGTCTGTAGTGGGAGTTTTCTTATGTGSCCTCCGACT 1811
Db 1670 AGNATAGCTACTGCCCCACCAAGTCTGTGTGGGGTTTTCTTATGCGGCCCTCCGACT 1729
QY 1812 TTGGCAAGAGCTGCGCAAAATGCTGTCAACCGATATTCAGTCTGGATCCTAGAAAGTT 1871
Db 1730 TTGGCAAAAGCTGCGCAAAATGCTGTGCGGCTACTCAAGTCTGGATCCTAGAAAGTT 1789
QY 1872 CAATTTCTACTTCAACAAAGAAATTTTTCAGTTATAGGAATAGGAGCGGTAAT 1924
Db 1790 CAATTTCTACTTCAACAAAGAAACGTTCTGATTTGGAGGAAGCGGCACAGTAGT 1842
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RESULT 11

US-10-318-906A-41

; Sequence 41, Application US/10318906A

; Publication No. US20030157678A1

; GENERAL INFORMATION:

; APPLICANT: Lambeth, J. David

; APPLICANT: Griendling, Kathy

; APPLICANT: Lassegue, Bernard

; APPLICANT: Arnold, Rebecca S.

; APPLICANT: Cheng, Guangjie

; TITLE OF INVENTION: Mitogenic Oxygenases

; FILE REFERENCE: 05501-0221

; CURRENT APPLICATION NUMBER: US/10/318,906A

; CURRENT FILING DATE: 2002-12-13

; PRIOR APPLICATION NUMBER: US 09/437,568

; NUMBER OF SEQ ID NOS: 61

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 41

; LENGTH: 2619

; TYPE: DNA

; ORGANISM: Rat

US-10-318-906A-41

Query Match 45.3%; Score 1182.8; DB 15; Length 2619;

Best Local Similarity 84.8%; Pred. No. 1.7e-291;

Matches 1338; Conservative 0; Mismatches 237; Indels 3; Gaps 1;

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QY 347 GTCAACATTTGGCTGTGCCCGAGCGTCTGCTCTCTGCTTGAATTTTAAACAGCACGCTGAT 406
Db 310 GACTGCCCTTGGCTTGGCCAGAGCATCTGCTTTGCGCTGAATTTTAAACAGCATGGTGT 369
QY 407 CTTGCTTCTGTGTGTCGAATCTGCTGCTTCTGAGGGGACCTGCTCATTTTTCAG 466
Db 370 CTTGATTTCTGTGTGTCGAATCTGCTTCTTCTGAGGGGACCTGCTCATTTTTCGAA 429
QY 467 CGCACACTGAGAGAGCAATTTGGATCAAACTCACCTCACAGCTTCCACAGCTGGTGGCCATAT 526
Db 430 CCAACGCTGAGAAAGCCATTTGGATCAAACTCACCTCACAGCTGGTGGGCGATATAT 489
QY 527 GATCTGCCATACATACAGCTATTTCATCATTTGCACACCTGTTTAACTTTTGACTGCTATAG 586
Db 490 GATCTGCATATTCAGCTATTTCATATTCATTCATTCATTTTAACTTTTGAACGCTACAG 549
QY 587 CAGAAAGCGGACAGGCGACAGATGGTCCCTTGGCTTCCATTTCTCTACGCTATCTCATGA 646
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Db 550 TAGAGCCACAGCCATGATGATCTCTTGCTCTGTTCTCTCCAGCCTATTCATCC 609
 Qy 647 TGAGAAAAAGGGGGTTCTTGGCTAAATCCATCCAGTCCGAAACACGACAGTGAGTA 706
 Db 610 CGAGAAA--GAAGATCTTGGCTAAATCCATCCAGTCCGAAACGACAGTGATGA 666
 Qy 707 TGTGACATTCACAGCGTCTGCTCTCACTGAGGTGATCATGACATGACATGCCCTGATCT 766
 Db 667 TGCAGCAATTCACAGTATCTGCGCCCTTACTGAGTGTGCGCACTGTGGCTTTGGTTCT 726
 Qy 767 CATGTAACCTTCAGTACTAGTTCATCCGAGAGAGTTATTTGAACTCTCTCGGTATAC 826
 Db 727 CATGTAACCTTCAGTATGAGTTATCCGAGGAATTTATTTGAGCTCTCTCGGTATAC 786
 Qy 827 TCACCACTTTTATCTTATATCTCTGCTTGGTTAGGATTCACGGCAATTCGTGGAATGT 886
 Db 787 ACATCACTTTTATCATCTATATCATCTGCTTAGGGATCCATGGCCCTGGGGGGATTTG 846
 Qy 887 CCGGGTCAACAGAGAGAGCATGAATGAGAGTCATCCTCGCAAGTGTGCAGAGTCTTT 946
 Db 847 CCGGGTCAACAGAGAGAGCATGAGTGAAGTCATCCCGCAACTGTTCTATCTCTTT 906
 Qy 947 TGAGATGTGGATGATCGTGACTCCCACTGTAGCGCCCTAAAGTTTGAAGGGCATCCCCC 1006
 Db 907 CCAGAGTGGATAAGTATGAAGAGTTCAGAGAGTCTCATTTTGTGGGCAACCCCC 966
 Qy 1007 TGAGTCTTGAAGTGGATCCCTTGACCGGTCAITCTTTTATATCTGTGAAAGATCCTCG 1066
 Db 967 TGAGTCTTGAAGTGGATCCCTCGCGCGATGCTTTTATATCTTTGAAAGGATCCTCG 1026
 Qy 1067 GTTTTACCGCTCCACAGAGAGGTGTGATTACCAAGTGTGTTATGACCCCATCCAAAGT 1126
 Db 1027 CTTTATTCGCTCCCGCAGAGGTGCTGATTAACAGTGTCTCATGACCCCATGTAAGT 1086
 Qy 1127 TTTGGAATGAGATGAACAAGCGTGGCTTCAGCATGGAAGTGGGGCAGTATATCTTTGT 1186
 Db 1087 TTTGGAATGAGATGAGGAAGCGGGCTTTACTATGGAATAGGACAGTATATATTCGT 1146
 Qy 1187 TAATGGCCCTCAATCTCTCTGGAATGGCATCTTTTACTTTGACCTCTGCTCCAGA 1246
 Db 1147 AAATTTGCCCTCGATTTCTTCTGGAATGGCATCCCTTTACTCTGACCTCTGCTCCAGA 1206
 Qy 1247 GGAAGATTTCTTCTCCATTCATATCCGAGCAGAGGGGACTGGACAGAAATCTCATAG 1306
 Db 1207 GGAAGATTTCTTCTCCATTCATATCCGAGCAGAGGGGACTGGACAGAAATCTCATAG 1266
 Qy 1307 GGCTTTGAAACAAATATTCACCAATTCAGGATGAAAGTGGATGCTCCCTTTGGAC 1366
 Db 1267 GACATTTGAAACAAAGCACTCACCAATGCCAGGATCGAGGTGGATGGTCCCTTTGGCAC 1326
 Qy 1367 AGCCAGTGAAGATCTTTTCCAGTATGAATGGCTGTGCTGGTGGAGCAGGAATTTGGGT 1426
 Db 1327 AGTCAGTGAGGATGTCTTCCAGTACGAAGTGGCTGTACTGGTTGGGGCAGGATTTGGGT 1386
 Qy 1427 CACCCCTTTCTCTATCTTGAATCCATCTGCTGACAAATTCAGTGTGACAGCAACAA 1486
 Db 1387 CACTCCCTTTCTTCTTGAATCTATCTGCTGACAAATTCAGCGTGCACACAA 1446
 Qy 1487 CCTCAAAACAAAAAGATCTATTTCTACTGATCTGAGGAGACAGTGTCTTTCTG 1546
 Db 1447 GCTGAAACACAAAAGATCTATTTCTACTGGATTTGTAGAGAGCGGGTGGCTTTG 1506
 Qy 1547 GTTCAACAACTGTGTCTCCCTGGAACAGAGATGGAGAAATTAGGCAAGTGGGTTT 1606
 Db 1507 GTTCAACAACTTATTTGAATTCCTTGGAAACAGAGATGGAGAAATTAGGCAACCGGATTT 1566
 Qy 1607 TCTAACTACCGTCTCTTCTTACCGGATGGGACAGCAATATTTGTTGCTCATGACGATTT 1666
 Db 1567 CTTAACTACCGTCTCTTCTTACCGGATGGGACAGCAATATTTGTTGCTCATGACGATTT 1626
 Qy 1667 AAATTTGACAGGCACTGATCTGTCAGAGTCTGAAACAGAAAACTCTCTTTGGAG 1726
 Db 1627 AAATTTGACAGGCACTGATCTGTCAGAGTCTGAAACAGAAAACTCTCTTTGGAG 1686

Qy 1727 ACCAATGTGGCAATGAGTCTTCTCAATAGTCTACTCCCAACCCCAAGTCTGTAGTGG 1786
 Db 1687 ACCAATGTGGCAATGAGTCTTCTCAATAGTCTACTCCCAACCCCAAGTCTGTAGTGG 1746
 Qy 1787 AGTTTTCTTATGTGGCCCTCGGACTTTGGCAAGAGAGCTCGCAAAATGCTGTCAACGATA 1846
 Db 1747 GGTTTCTTATGTGGCCCTCGGACTTTGGCAAGAGAGCTCGCAAAATGCTGTGCGGATA 1806
 Qy 1847 TTCAGTCTGGATCTCTAGAAAGTTCATTTCTACTTCAACAAAGAAATTTTGTAGTTAT 1906
 Db 1807 CTCAGTCTGGATCTCTAGAAAGTTCATTTCTACTTCAACAAAGAAACGTTCTGATTTG 1866
 Qy 1907 AGGAATGAAGACGTAAT 1924
 Db 1867 AGGAAGCCGACAGTAGT 1884

RESULT 12
 US-10-319-236A-41
 ; Sequence 41, Application US/10319236A
 ; Publication No. US20030166198A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lambeth, J. David
 ; APPLICANT: Griendling, Kathy
 ; APPLICANT: Lassegue, Bernard
 ; APPLICANT: Arnold, Rebecca S.
 ; APPLICANT: Cheng, Guangjie
 ; TITLE OF INVENTION: Antibodies to Mitogenic Oxygenases
 ; FILE REFERENCE: 05501-0220 (43150-281176)
 ; CURRENT APPLICATION NUMBER: US/10/319,236A
 ; CURRENT FILING DATE: 2002-12-13
 ; PRIOR APPLICATION NUMBER: US 09/437,568
 ; PRIOR FILING DATE: 1999-11-10
 ; NUMBER OF SEQ ID NOS: 61
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 41
 ; LENGTH: 2619
 ; TYPE: DNA
 ; ORGANISM: Rat
 US-10-319-236A-41

Query Match 45.3%; Score 1182.8; DB 15; Length 2619;
 Best Local Similarity 84.8%; Pred. No. 1.7e-291;
 Matches 1338; Conservative 0; Mismatches 237; Indels 3; Gaps 1;

Qy 347 GTCAACATTTGGCTGTGTCGCGAGGCTGTGCTCTGCTTGAATTTTAAACAGCAGCTGAT 406
 Db 310 GACTGCTTTGGCTTTGGCCAGAGCATCTGCTTTGCTGCTGAATTTTAAACAGCAGCTGAT 369
 Qy 407 CCTGCTTCTGTGTGTCGCAATCTGCTCTCTGAGGGGACCTGCTCATTTTTCAG 466
 Db 370 CCTGATTTCTGTGTGTCGCAATCTGCTCTCTGAGGGGACCTGCTCATTTTTCAG 429
 Qy 467 CCGCACACTGAGAAAGCAATTTGGATCAACCTCACCTTCCAAAGCTGGTGGCTATAT 526
 Db 430 CCACAGCTGAGAAAGCAATTTGGATCAACCTCACCTTCCATTAAGCTGGTGGCATATAT 489
 Qy 527 GATCTGCTATACACAGTATTTACATCATTTGACACCTGTTTAACTTTGACTGCTATAG 586
 Db 490 GATCTGATATTTACAGCTATTTATATCATTTGCAATCTATTTAACTTTGAAACGCTACAG 549
 Qy 587 CAGAAGCCGACAGAGATGGCTCCCTGCTCCATTTCTTCCAGCCCTATCTCATGA 646
 Db 550 TAGAAGCCACAGGCGCATGGATGGATCTTTGCTCTGTTCTCTCCAGCTTATTTCCATCC 609
 Qy 647 TGAGAAAAAGGGGTTCTTGGCTTAAATCCATCCAGTCCCGAAACACAGAGTGGAGTA 706
 Db 610 CGAGAAA--GAAGATTTCTTGGCTAAATCCCATCCAGTCTCCAAACGTTGACAGTATGA 666
 Qy 707 TGTGACATTCACAGCGTGTGCTGCTCACTGGAGTATCATGACAAATAGCTTCTGATTTCT 766
 Db 667 TGCAGCATTTTACAGTATTTGCTGGCTTACTTGGAGTGGTCCGCACTGTGGCTTTGGTTCT 726

QY 767 CATGGTAACCTCAGCTACTGAGTTTCATCCGAGAGATTATTTTGAAGTCTTCTGGTATAC 826
Db 727 CATGGTAACCTCAGCTACTGAGTTTATCCGAGAGATTATTTTGAAGTCTTCTGGTATAC 786
QY 827 TCACCAACCTTTTATCTCTCTATATCCTTGTGCTTAGGGATTCACGGCAATTGGTGGAAATTGT 886
Db 787 ACATCACTTTTTCATCATCTATATCATCTCTTAGGGATCCATGGCCCTGGGGGGGATTTGT 846
QY 887 CCGGGTCAACAGAGAGAGAGCATGAATGAGATCATCTCGCAAGTGTGCAGAGTCTTT 946
Db 847 CCGGGTCAACAGAGAGAGAGCATGAGTGAAGTCATCCCGCAACTGTTTCATACTCTTT 906
QY 947 TGAGATGTGGGATGATCGTGACTCCCACTGTAGCGGCCCTTAAGTTTGAAGGGCATCCCC 1006
Db 907 CCAGAGTGGGATGAAGTATGAAGGAGTTGACAGAGTCTTCATTTTGTGGGGCAACCCCC 966
QY 1007 TGAGTCTTGGAGTGGATCCTTGCACCGGTCAITCTTTATATCTGTGAAGAGTCTCCG 1066
Db 967 TGAGTCTTGGAGTGGATCCTCGCGCGATGCTTTTATATCTTTGAAGAGTCTCTCG 1026
QY 1067 GTTTTACCGTCCAGAGAGGTTGTGATTACCAAGTTGTATGCAACCCCATCCAAAGT 1126
Db 1027 CTTTATCGTCCCGCAGAGGCTGTGATTACCAAGTTGTTCATGCACCCATGTAAAGT 1086
QY 1127 TTTGGAATTCAGATGAACAAGCGTGGCTTCAGCATGGAAGTGGGCGAGTATATCTTGT 1186
Db 1087 TTTGGAATTCAGATGAGGAAGCGGGCTTTTACTATGGAATAGGACAGTATATTCGT 1146
QY 1187 TAAATGCCCCCTCAATCTCTCTCGAATGGCATCTTTTACTTTGACCTCTGCTCCAGA 1246
Db 1147 AATATGCCCCCTCGATTCCTCTCGAATGGCATCTTTTACTTCGACCTCTGCTCCAGA 1206
QY 1247 GGAAGATTTCTTCTCATTCATATCCAGCAGCAGGGGACTGGACAGAAAACTCATAG 1306
Db 1207 GGAAGAAATTTTCTCCATTCATATCCAGCAGCAGGGGACTGGACAGAAAACTCATAG 1266
QY 1307 GCGTTTCGACACACATATTCACCAATTCAGGATTTGAAGTGGATGGTCCCTTGGAC 1366
Db 1267 GACATTTGAACACACAGCATCCACCAATGCCAGGATCGAGGTGGATGGTCCCTTTGGCAC 1326
QY 1367 AGCCAGTGAAGATGTTTTCCAGTATGAAGTGGCTGTGCTTGGAGCAGGAAATGGGGT 1426
Db 1327 AGTCAGTGAAGATGCTTCCAGTACGAAGTGGCTGTGCTTGGAGCAGGAAATGGGGT 1386
QY 1427 CACCCCTTTGCTTCTATCTTGAATTCATCTGGTACAAATTCAGTGTGCAGACCAAA 1486
Db 1387 CACTCCCTTTGCTTCTTGAATTCATCTGGTACAAATTCAGCGGTGCACACAA 1446
QY 1487 CCTCAAAACAAAAGATCTATTTCTACTGGATTCGAGGATGAGAGACGGGTGGCTTTGCCG 1546
Db 1447 GCTGAANAACAAAAGATCTATTTCTACTGGATTTGTAGAGACGGGTGGCTTTGCCG 1506
QY 1547 GTTCAACAACTGTTGACTTCCCTGGAACAGAGATGGAAGAAATAGGCAAGTGGGTTT 1606
Db 1507 GTTCAACAACTTATGAATTCCTTGAACAGAGATGGAAGAAATAGGCAACCGGATTT 1566
QY 1607 TCTAACTACCGTCTCTCCTCACCGGATGGGACAGCAATATGTTGGTTCATGAGCAAT 1666
Db 1567 CCTAAACTACCGACTCTTCTCACTGGCTGGATAGCAACATTTGCTGGTTCATGCAAT 1626
QY 1667 AAACCTTGCAGAGGCCACTGACATCGTACAGGCTGTGAACAGAAACCTCTTTGGGAG 1726
Db 1627 AAACCTTGCAGAGGCCACTGACGCTGTGACAGGCTGTGAACAGAAACCTCTTTGGGAG 1686
QY 1727 ACCAATGTGGGACAATGAGTTTTCTACAAATAGTACTCTCCACCCCAAGTCTGTAGTGG 1786
Db 1687 ACCAATGTGGGACAATGAGTTTTCTAGATAGTACTGCCCACCCCAAGTCTGTGGTGG 1746
QY 1787 AGTTTTCTTATGTGGCCCTCGGATTTTGGCAAGAGCCCTGGCACAATGCTGTACCGATA 1846
Db 1747 GGTTTTCTTATGCGGCCCTCCGACTTTGGCAAAAGCCCTGGCACAATGCTGTCCGCGTA 1806

QY 1847 TTCAGTCTGGATCTTAGAAGGTTCAATTCTACTTCAACAAAGAAAAATTTTTCAGTTAT 1906
Db 1807 CTCAAGTCTGGATCTTAGAAGGTTCAATTCTACTTCAACAAAGAAACGTTCTGAAATGG 1866
QY 1907 AGGAATAAGACGGTAAT 1924
Db 1867 AGGAAGCCGCACAGTAGT 1884

RESULT 13

US-10-618-839-15

; Sequence 15, Application US/10618839

; Publication No. US20040093628A1

; GENERAL INFORMATION:

; APPLICANT: Lambeth, J. David

; APPLICANT: Cheng, Guangjie

; APPLICANT: McCoy, James

; TITLE OF INVENTION: Methods and Transgenic Mouse Model for Identifying and Modulating

; TITLE OF INVENTION: Factors Involved in the Production of Reactive Oxygen

; FILE REFERENCE: 05501-0211 (43150-286808)

; CURRENT APPLICATION NUMBER: US/10/618,839

; CURRENT FILING DATE: 2003-07-14

; PRIOR APPLICATION NUMBER: US 60/395,498

; PRIOR FILING DATE: 2002-07-12

; NUMBER OF SEQ ID NOS: 19

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 15

; LENGTH: 797

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthetic primer

US-10-618-839-15

Query Match

Best Local Similarity 30.5%; Score 797; DB 17; Length 797;

Matches 797; Conservativity 100.0%; Pred. No. 4.5e-193;

Mismatches 0; Indels 0; Gaps 0;

QY 1065 CGGTTTACCGCTCCCGCAGCAGAGGTTGTGATTACCAAGTTGTTATGCACCCATCCAA 1124

Db 1 CGGTTTACCGCTCCCGCAGCAGAGGTTGTGATTACCAAGTTGTTATGCACCCATCCAA 60

QY 1125 GTTTTGAATTCAGATGAACAAGGTTGGCTTCAGCATGGAAGTGGGCGAGTATATCTTT 1184

Db 61 GTTTTGAATTCAGATGAACAAGGTTGGCTTCAGCATGGAAGTGGGCGAGTATATCTTT 120

QY 1185 GTTAATGGCCCTCAATCTCTCTCTGGAATGGCATCCCTTTTACCTTGACCTCTGCTCA 1244

Db 121 GTTAATGGCCCTCAATCTCTCTCTGGAATGGCATCCCTTTTACCTTGACCTCTGCTCA 180

QY 1245 GAGGAAGATTTCTTCTCCATTCATATCCGAGCAGAGGGGACTGGACAGAAATCTCATA 1304

Db 181 GAGGAAGATTTCTTCTCCATTCATATCCGAGCAGAGGGGACTGGACAGAAATCTCATA 240

QY 1305 AGGGCTTTTGAACAACAATATTCACCAATTCAGATGGAAGTGGTCCCTTTGGC 1364

Db 241 AGGGCTTTTGAACAACAATATTCACCAATTCAGATGGAAGTGGTCCCTTTGGC 300

QY 1365 ACAGCAGTGGAGATGTTTCCAGTATGAAGTGGCTGTGCTGGTGGAGCAGAAATGGG 1424

Db 301 ACAGCAGTGGAGATGTTTCCAGTATGAAGTGGCTGTGCTGGTGGAGCAGAAATGGG 360

QY 1425 GTACCCCTTTGCTTCTATCTTGAATCCATCTGGTACAAATCCAGTGTGCAGACAC 1484

Db 361 GTACCCCTTTGCTTCTATCTTGAATCCATCTGGTACAAATCCAGTGTGCAGACAC 420

QY 1485 AACCTCAAAACAAAAGATCTATTTCTACTGGATCTGCAGGAGACAGGTGCCTTTTCC 1544

Db 421 AACCTCAAAACAAAAGATCTATTTCTACTGGATCTGCAGGAGACAGGTGCCTTTTCC 480

QY 1545 TGGTTCAACAACTGTTGACATTCCTTGGAAACAGGAGTGGAGGAATTAGGCAAAAGTGGT 1604

Db 481 TGGTTCAACACCTGTTGACTTCCCTGGAACAGAGATGAGGAAATAGGCAAGTGGT 540
 Qy 1605 TTCTAAACTACCGTCTCTTCTCCTCACCGGATGGACAGCAATATGTTGGTCAATGACGA 1664
 Db 541 TTCTAAACTACCGTCTCTTCTCCTCACCGGATGGACAGCAATATGTTGGTCAATGACGA 600
 Qy 1665 TTAAACTTTGACAGGCGCACTGACATGTCGACAGGCTGGAACAGAAACCTCTTTGGG 1724
 Db 601 TTAAACTTTGACAGGCGCACTGACATGTCGACAGGCTGGAACAGAAACCTCTTTGGG 660
 Qy 1725 AGACCAATGCGGCAATAGTATTTCTACCAATAGCTACCTCCCAACCAAGTCTGTAGTG 1784
 Db 661 AGACCAATGCGGCAATAGTATTTCTACCAATAGCTACCTCCCAACCAAGTCTGTAGTG 720
 Qy 1785 GGAGTTTCTTATGATGCGCCCTCGGACTTTGGCAAAAGCGCTGCGCAAAATGCTGTCACGA 1844
 Db 721 GGAGTTTCTTATGATGCGCCCTCGGACTTTGGCAAAAGCGCTGCGCAAAATGCTGTCACGA 780
 Qy 1845 TATTCAGTCTGGATCC 1861
 Db 781 TATTCAGTCTGGATCC 797

RESULT 14

US-10-342-887-480
 ; Sequence 480, Application US/10342887
 ; Publication No. US20040058340A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dai, Hongyue
 ; APPLICANT: He, Yudong
 ; APPLICANT: Linsley, Peter S.
 ; APPLICANT: Mao, Mao
 ; APPLICANT: Roberts, Christopher J.
 ; APPLICANT: Van 't Veer, Laura Johanna
 ; APPLICANT: Van de Vijver, Marc J.
 ; APPLICANT: Bernards, Rene
 ; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
 ; FILE REFERENCE: 9301-188-999
 ; CURRENT APPLICATION NUMBER: US/10/342,887
 ; CURRENT FILING DATE: 2003-01-15
 ; PRIOR APPLICATION NUMBER: 60/298,918
 ; PRIOR FILING DATE: 2001-06-18
 ; PRIOR APPLICATION NUMBER: 60/380,710
 ; PRIOR FILING DATE: 2002-05-14
 ; PRIOR APPLICATION NUMBER: 10/172,118
 ; PRIOR FILING DATE: 2002-06-14
 ; NUMBER OF SEQ ID NOS: 2699
 ; SEQ ID NO 480
 ; LENGTH: 4266
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-342-887-480

Query Match 22.3%; Score 582; DB 13; Length 4266;
 Best Local Similarity 60.0%; Pred. No. 1.6e-137;
 Matches 1035; Conservative 0; Mismatches 665; Indels 24; Gaps 3;
 Qy 204 ACAATGGAACTGGTGGTTAAACCACCTGGTTTTCAGTTTGTCTGGTTGTTGTTA 263
 Db 12 ACCATGGGAACTGGGCTGTGAATGAGGGCTCTCCATTTTGTCAITCTGGTTGGCTG 71
 Qy 264 GGGCTGAATGTTTCTGTTTGTGGATGCTCTCTGAAATATGAGAGGCCGACAAATAC 323
 Db 72 GGGTTGAACGCTTCTCTTGTCTGTTATACCGGGTTATGATATTCACCTAAGTTC 131
 Qy 324 TACTACACAGAAAAATCCTTTGGTCAACATTTGGCTGTGCGGAGCGTCTGTCTCTGC 383
 Db 132 TTTTACACAGAAAACTCTTTGGGTACAGCACTGGCACTGGCGAGGCGCCCTGCACGCTGC 191
 Qy 384 TTGAATTTTACAGACGCTGATCTGCTTCTGTGTGTCGCAATCTGCTGCTTCTGCTG 443
 Db 192 CTGAATTTCACTGATGCTGATCTCTTGGCAGTCTGTGAAATCTGCTGCTTCTCTC 251

Qy 444 AGGGGCACTGCTCATTTTTCAGCGCACACTGAGAAAGCAATTTGGATCACAACCTCACC 503
 Db 252 AGGGGTTCCAGTTCGCTGCTCTCAACAGAGTTTGAAGACAACTGGACAGATCTCACC 311
 Qy 504 TTCCACAAGCTGTGGCTTATATGCTGCTACATACAGCTTATTCACATCATTTGCACAC 563
 Db 312 TTTTCATAAATGTTGGCATGATGTCACCTTCTACTCTCGGATTCACCAATTCACAT 371
 Qy 564 CTGTTTAACTTTGACTGCTATAGAGAAAGCGGACAGCCACAGATGCTCCTTTGCTCC 623
 Db 372 CTATTTAAATGTTGAATGCTGTGAATGCGCGAGTCAATAATTTCTGATCCTTATTCAGTA 431
 Qy 624 ATTTCTCTCCAGCTTATCTCATGATGAGAAAGGGGGTTCTTGGCTAAATCCCATCCAG 683
 Db 432 GCATCTCTCGAATTTGGAGACAGGCAAAATGAAGTTATCTCAATTTTGTTCGAAAGAGA 491
 Qy 684 TCCGAAACACGACAGTGG---AGTATGTGACATTTCCACAGCGTGTGCTGCTCCTGGA 740
 Db 492 ATAAAGAAACCTGAAGGAGGCTGTACTCGCTGTGACCTGTGTCAGGAGCATCCTGGA 551
 Qy 741 GTGATCATGACATAGCTTGAATCTCATGTTAACTTCACTACTGAGTTCATCCGAGG 800
 Db 552 GTTGTCACTACGCTGTGCTCATATTAATTAATCACTTCTCCCAAAACCATTCGGAGG 611
 Qy 801 AGTTATTTTGAAGTCTTCTGCTATATCAACACACCTTTTATCTTCTATATCTTGGCTTA 860
 Db 612 TCTTACTTTGAGTCTTTTGGTACACATCACTCTTGTGATCTTCTTCAATTTGGCTT 671
 Qy 861 GGGATTCACGGCATTTGTTGGAATTTGTCGGGGTCAAAACAGAGGAGAGATGAATGAGAT 920
 Db 672 GCCATCCATGGAGCTGAACGAATTTGACGTGGGCGAGACCGCAGAGAGTTTGGCTGTGCAT 731
 Qy 921 CATCTCGCAAGTGTGAGAGTCTTTTGAATGTTGGGATGATCTGTAATCCCATCTGAGG 980
 Db 732 AATATAACAGTTTGTGAACAAAAAATCTCAGAATGGGGGAAAAATAA---GGAATGCCCA 788
 Qy 981 CGCCCTAAGTTTGAAGGGGCTTCCCTCTGAGTCTTGGAAAGTGGATCTTTCACCGGTCATT 1040
 Db 789 ATCCCTCAGTTTCTGGAACCCCTCTTATGACTTGGAAATGGATAGTGGGTCCCATGTTT 848
 Qy 1041 CTTTATATCTGTGAAAGGATCTCCGGTTTACCGTCTCCAGCAGAGAGAGTGTGATTAACC 1100
 Db 849 CTGTATCTCTGAGAGGTTGGTGGGTTTGGCGGATCTCAACAGAAAGTGTGTCATCACC 908
 Qy 1101 AAGGTTCTATGACACCATCCAAAGTTTGGAAATTTGCAGATGAACAGCGTGGCTTACG 1160
 Db 909 AAGTGTGCTACTCACCCTTTCAAAACCATCGAGTACAGATGAAGAAGAGGGGTTCAAA 968
 Qy 1161 ATGGAAGTGGGCGAGTATATCTTTTGTAAATTTGCCCTCAATCTCTCTCTGGAATGGCAT 1220
 Db 969 ATGGAAGTGGGCAATACATTTTGTCAAGTGCCCAAGGTTGTCCAAGCTGAGTGGCAC 1028
 Qy 1221 CTTTATATTTGACCTCTGCTCCAGAGAGATTTCTTCTCCATTCATATCCGAGCAGCA 1280
 Db 1029 CTTTATACCTACATCCGCCCTCTGAGGAAGACTTCTTAGTATCCATATCCGATCGTT 1088
 Qy 1281 GGGGACTGGACAGAAATCTCATAGGCTTTTCG-----AACAACAA 1322
 Db 1089 GGGGACTGGACAGAGGGGCTGTTCAATGCTTGTGGTGTGATAAGCAGGAGTTTCAAGAT 1148
 Qy 1323 TATTACCAATTTCCAGGATTTGAAGTGGATGGTCCCTTTGGCAGCGAGTGTGAGATGTT 1382
 Db 1149 GCGTGGAAACTTACCTAAGATAGCGGTTGATGGGCTTTGGGCACTGCGCAGTGAAGATGTG 1208
 Qy 1383 TTCAGATATGAATGGGCTGTGCTGTTGGAGCAGAAATTTGGGTCACCCCTTGTCTTCT 1442
 Db 1209 TTCAGCTATGAGTGGTGTGATTTAGTGGGAGCAGGATTTGGGTCACACCTTTCGATCC 1268
 Qy 1443 ATCTTGAATTCATCTGTCATAAATTTCCAGTGTGAGACCAACCAACCTCAAAACAAAAAG 1502
 Db 1269 ATTCTCAAGTCACTGTGTACAAATATTTGCAATTAAGCCCAACCAATCTGAAGCTCAAAAG 1328
 Qy 1503 ATCTATTTCTATCTGATCTGAGGAGACAGGTGCTTTTCTGTTTCAACAACTGTTG 1562

Db 1329 ATCTTACTTCTACTGGCTGTGCGGGACACACATGCTTGTGAGTGGTTGCGAGTCTGCTG 1388
Qy 1563 ACTTCCCTGGAAACAGGAGATGGAGGAATTAGGCAAGTGGGTTTTCTAAACTACCGTCTC 1622
Db 1389 CAAGTGTGGAGAGCCAGATGCGAGAAAGGAACAATGCCGGCTTCTCAGCTCAACATC 1448
Qy 1623 TTCTCTACCGGATGGGACAGCAATATTGTTGGTCTATGCGACATTAATTAATTTGACAAGGCC 1682
Db 1449 TACTCTACTGGCTGGGATGAGTCTCAGGCCAATCACTTGTGTCACCATGATGAGGAG 1508
Qy 1683 ACTGACATCGTGACAGTCTGAACAGAAAAACCTCTTTGGGAGACCAATGTGGGCAAT 1742
Db 1509 AAAGATGTGATCAGAGCCCTGAAACAAAGACITTTGATGAGCGGCCCACTGGGATAAT 1568
Qy 1743 GAGTTTCTACAATAGTACTCTCCACCACCAAGTCTGTAGTGGAGTTTTCTTATGTGGC 1802
Db 1569 GAATTTCAAGCAATGCAAGTCAACACCCTAATACCAGAAATAGGAGTTTTCTCTGTGGA 1628
Qy 1803 CCTCGGACTTTGGCAAGAGCCTGCGCAATGCTGTCAACCGATATTCCAGTCTGGATCCT 1862
Db 1629 CTTGAAGCCTTGGTGAAACCCCTGAGTAAACAAAGCAATCTCAACTCTGAGTCTGGCCCT 1688
Qy 1863 AGAAAGTTCAATTTCTACTTCAACAAAGAAAAATTTTGTAGTTAT 1906
Db 1689 CGGGAGTGCATTTCTATTTTCAACAGAAAACTTCTAACTTGT 1732

RESULT 15

US-10-172-118-480
; Sequence 480, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10/172,118
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 480
; LENGTH: 4266
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NM 000397
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-480

Query Match 22.3%; Score 582; DB 13; Length 4266;
Best Local Similarity 60.0%; Pred. No. 1.6e-137;
Matches 1035; Conservative 0; Mismatches 665; Indels 24; Gaps 3;
Qy 204 ACAATGGGAAACTGGGTGGTTAAACCACTGGTTTTCAGTTTTTCTGTTTCTGTTTGGTTA 263
Db 12 ACCATGGGAACTGGGCTGTGATGAGGGGCTCTCCATTTTGTCAATCTGTTTGGTGTG 71
Qy 264 GGGCTGAATGTTTTCTGTTTGTGGATGCCCTTCTGAATATGAGAAGGCCGACAAATAC 323
Db 72 GGGTTGAACGTCTCTCTTTTGTCTGTTATTACCGGTTTATGATATCCACTAAGTTC 131
Qy 324 TACTACAGAAAAAATCTTGGGTCAACATTTGGGCTGTGCCCGGCGGTCTCTCTCTG 383
Db 132 TTTTACAGAAAAAATCTTGGGTGAGCACTGGCACTGGCCAGGCGCCCTGACGCTCTG 191

Qy 384 TTGAATTTTAAACAGCAGCGTGAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTG 443
Db 192 CTGAATTTTCAACTGCATGCTGATTCTCTTCCAGTCTGTGGAAATCTGCTGTCTCTCTCTC 251
Qy 444 AGGGCACCCTGCTCATTTTTCAGCCGCACACTGAGAAAGCAATTTGATTCACACCTCAC 503
Db 252 AGGGTTTCCAGTGGCTGCTCTCAACAAGATTTGGAAGACAACCTGGACAGGAATCTCAC 311
Qy 504 TTCCACAAGCTGGTGGCTATATGATCTGCTACATACAGCTATTTCATCATTCATTCACAC 563
Db 312 TTTTCAATAAATGGTGGATGGATGATTGCACTTCACTCTCGGATTTACACATTTGACAT 371
Qy 564 CTGTTTAACTTTGACTGCTATAGCAGAAAGCCGACAGCCACAGATGCTCTCTCTCTCTCT 623
Db 372 CTATTTAAATGGAATGGTGTGTAATGCCGAGTCAATAATTTCTGATCTCTTATTCAGTA 431
Qy 624 ATTCTCTCCAGCTATCTCATGATGAGAAAAAGGGGGTTCTTGGGTGTAATTCATCCAC 683
Db 432 GCACCTCTGAACTTGGAGACAGGCAAAATGAAAGTTATCTCAATTTTGTGCGAAAGAGA 491
Qy 684 TCCGAAAACACGACAGTGG---AGTATGTGACATTCACACAGCGTTGCTGCTCTCACTGGA 740
Db 492 ATAAAGAACCTTGAAGAGGSCCTGTACCTGGCTGTGACCTGTTGGCAGGCATCACTGGA 551
Qy 741 GTGATCATGACAATAGCCTTTGATTTCTCATGGTAACTTTCAGCTACTGAGTTTCATCCGAG 800
Db 552 GTTGTCAATCACGCTGTGCTCTCATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 611
Qy 801 AGTTATTTTGAAGTCTTCTGGTATCTCAACACCTTTTATCTCTATCTCTCTCTCTCTCT 860
Db 612 TCTTACTTGAAGTCTTTTGGTACACACATCATCTCTTTGTGATCTCTTCTTCTTCTTCT 671
Qy 861 GGGATTCAAGCGCATTTGGTGAATTTGCCGGGGTCAACAGAGGAGAGCATGAATGAGAT 920
Db 672 GCCATCCATGAGCTGAACGAATTTGACGTGGCAGACCGCAGAGAGTTTGGCTGTGCAT 731
Qy 921 CATCTCGCAAGTGTGCAGAGTCTTTTGGAGATGTGGGATGATCGTGACTCCCACTCTGAG 980
Db 732 AATATAACAGTTTGTGAACAAAAAATCTCAGAATGGGAAAAATAAA---GGATGCCCA 798
Qy 981 CGCCCTAAAGTTGAAGGGCATCCCCCTGAGTCTTGGAAAGTGAATCTCTGACCGGTCATT 1040
Db 789 ATCCCTCAGTTTGTGGAAACCTCTCTATGACTTGGAAATGAGTAGTGGGTCCCATGTTT 848
Qy 1041 CTTTATATCTGTGAAGGATCTCTCGGTTTATACCGCTCCAGCAGAAAGTGTGTGATTACC 1100
Db 849 CTGTATCTCTGTGAGAGGTTGGTGGGTTTGGCGATCTCAACAGAGAGTGGTTCATCACC 908
Qy 1101 AAGGTTGTTATGCACCCATCCAAAGTTTGGAAATTCAGATGAACAAGCGTGGCTTCAGC 1160
Db 909 AAGGTGGTCACTCACCCCTTTCAAAACCATCGAGCTACAGATGAAGAAGAGGGTTCAAA 968
Qy 1161 ATGGAAAGTGGGCGAGTATATCTTGTGTAATTCGCCCTCAATCTCTCTCTGGAATGGCAT 1220
Db 969 ATGGAAAGTGGGACAATACATTTTGTCAAGTCCCAAGGTGTCCAAGCTGGAGTGGCAC 1028
Qy 1221 CTTTTTACTTTGACCTCTGCTCCAGAGGAAGATTCTTCTCCATTCATATCCGACGACGA 1280
Db 1029 CTTTTTACACTGACATCGCCCTCGAGGAAGACTTCTTTAGTATCCATATCCGATCGGTT 1088
Qy 1281 GGGGACTGGACAGAGGGGCTGTTCAAATGCTTGTGGCTGTGATAGCAGAGTTTCAAGAT 1322
Db 1089 GGGGACTGGACAGAGGGGCTGTTCAAATGCTTGTGGCTGTGATAGCAGAGTTTCAAGAT 1148
Qy 1323 TATTCACCAATTTCCAGGATGAAGTGAATGGTCCCTTTGGCAGACCGCAGTGAAGATGTT 1382
Db 1149 CGGTGGAAACCTACCTAAGATAGCGGTTGATGGGCCCTTTGGCAGCTGCCAGTGAAGATG 1208
Qy 1383 TTCCAGTATGAAGTGGCTGTGCTGGTGGAGCAGGAATTTGGGTCCACCCCTTTGCTTCT 1442
Db 1209 TTCAGCTATGAGTGGTGAATGTTAGTGGAGCAGGAGTTGGGGTTCACACCTTTGCACTC 1268
Qy 1443 ATCTTGAATTCATCTGTGTAATAATTCAGTGTGAGACCAACACCTCAAAACAAAAAG 1502

Db	1269	ATTCTCAAGTCAGTCTGGTACAAATATTGCAATAACGCCACCAATCTGAAGCTCAAAAAG	1328
Qy	1503	ATCTATTCTACTGGATCTGCAGGGAGACAGGTGCTTTTCTGGTTCAACAACCTGTTG	1562
Db	1329	ATCTACTTCTACTGGCTGTGCGGGACACACATGCCCTTTGAGTGGTTTGCAGATCTGCTG	1388
Qy	1563	ACTTCCCTGGAAACAGGAGATGGAGGAATTAGGCHAAAGTGGGTTTCTAAACTACCGTCTC	1622
Db	1389	CAACTGCTGGAGAGCCAGATGCAGGAAAGGAACAATGCCGGCTTTCCTCAGCTACAAATC	1448
Qy	1623	TTCTCTACCGGATGGGACAGCAATATTGTTGGTCAATGCAGCATTAATACTTTGACAAGGCC	1682
Db	1449	TACCTCACTGGCTGGGATGAGTCTCAGGCCAATCACTTTGCTGACCAATGATGAGGAG	1508
Qy	1683	ACTGACATCGTGCAGGTCTGAACAGAAAAACCTCTTTGGGAGACCAATGTGGACAAT	1742
Db	1509	AAAGATGTGATCA CAGGCTGAAACAAAAGACTTTGTATGGACGGCCCAACTGGGATAAT	1568
Qy	1743	GAGTTTCTCAATAGCTACCTCCACCCCAAGTCTGTAGTGGAGTTTCTTATGTGGC	1802
Db	1569	GAATTCAGACAATTGCAAGTCAACACCCTAATACCAGATAGGAGTTTCTCTGTGGA	1628
Qy	1803	CCTCGGACTTTGGCAAGAGCCTGGCAATATGCTGCACCGATATTCCAGTCTGGATCCT	1862
Db	1629	CCTGAAGCCTTGGCTGAAACCTGAGTAAACAAGCATCTCCAATCTGTAGTCTGGCCT	1688
Qy	1863	AGAAAGTTCAATTCTACTCAACAAAGAAAAATTTTGGATTAT	1906
Db	1689	CGGGAGTGCATTTTCATTTTCAACAAGGAAAACTTCTAACTGT	1732

Search completed: July 23, 2004, 13:47:58
Job time : 1153 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 23, 2004, 07:28:50 ; Search time 6455 Seconds
(without alignments)
12069.780 Million cell updates/sec

Title: US-10-618-839-1

Perfect score: 2609

Sequence: 1 gctgatagcacagtctgtc.....aaaaaaaaaaaaaaaaaaaaa 2609

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estnu:*

5: em_estcov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inh:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_pbg:*

27: em_gss_vrl:*

28: gb_gsl:*

29: gb_gsl2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1454.4	55.7	1695	29	AY403530
2	1251.2	48.0	1695	29	AY403531
3	1108.6	42.5	1689	29	AY403532
4	658.6	25.2	668	10	AW850622

5	644.8	24.7	665	10	AW377012
6	633.2	24.3	652	10	AW604216
7	614.8	23.6	618	10	AW850616
c	614.6	23.6	695	10	AW752752
9	605.4	23.2	607	10	AW604206
10	601.8	23.1	618	10	AW850625
11	597.2	22.9	605	10	AW604209
12	584	22.4	3242	11	AK053920
13	580.6	22.3	588	10	AW376980
14	580	22.2	4000	11	BC042838
15	579.8	22.2	583	10	AW850699
16	577.8	22.1	3925	11	AK033570
17	577.2	22.1	605	10	AW604208
18	576.8	22.1	592	10	AW604284
19	559	21.4	559	10	AW604166
20	555.4	21.3	575	10	AW376972
21	546.4	20.9	564	10	AW376901
22	545	20.9	561	10	AW752748
23	541	20.7	541	10	AW376979
24	536.4	20.6	538	10	AW376866
c	534.8	20.5	608	10	AW604199
26	533.8	20.5	545	10	AW376968
27	527.6	20.2	545	10	AW377061
c	524.8	20.1	584	13	BQ325148
29	512.2	19.6	517	10	AW604210
30	508.4	19.5	740	10	AW850619
31	503.2	19.3	510	10	AW377032
c	496.4	19.0	569	10	AW376900
33	492	18.9	563	10	AW604198
c	491	18.8	588	10	AW850690
35	484.4	18.6	542	10	AW376963
36	483	18.5	483	13	BX281577
c	482.6	18.5	572	10	BF591415
38	480.4	18.4	567	10	AW604168
c	479.8	18.4	532	9	AA587368
40	452.8	17.4	540	9	AI791894
c	446.4	17.1	593	9	AI821410
42	443.4	17.0	645	10	AW850617
43	442.4	17.0	710	10	BF334092
c	441.6	16.9	531	10	AW376895
c	436.8	16.7	556	10	AW604218

ALIGNMENTS

RESULT 1	AY403530	Homo sapiens NOX1 gene, genomic survey sequence.	1695 bp	DNA linear	GSS 15-DEC-2003
LOCUS	AY403530	Genomic survey sequence.			
DEFINITION	AY403530.1	GI:39759513			
ACCESSION	AY403530	GSS.			
VERSION	AY403530.1	GSS.			
KEYWORDS		Homo sapiens (human)			
SOURCE		Homo sapiens			
ORGANISM		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE	1	(bases 1 to 1695)			
AUTHORS		Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.			
TITLE		Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios			
JOURNAL	Science	302 (5652), 1960-1963 (2003)			
PUBMED	14671302				
REFERENCE	2	(bases 1 to 1695)			
AUTHORS		Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.			
TITLE		Direct Submission			

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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Best Local Similarity 85.8%; Pred. No. 6.1e-212;
Matches 1455; Conservative 0; Mismatches 240; Indels 0; Gaps 0;
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Qy 327 TACACAGAAATAATCCTGGGTCAACATGGCTGTCGCCGAGCGTCTCTCTGCTTG 386
Db 121 TACACAGAAATAATCCTGGGTCAACATGGCTGTCGCCGAGCGTCTCTCTGCTTG 180
Qy 387 AATTTTAAACAGCAGCTGATCCTGCTTCCTGTGTGCGCAATTCGTGTCCTTCCTGAGG 446
Db 181 AATTTTAAACAGCAGCTGATCCTGCTTCCTGTGTGCGCAATTCGTGTCCTTCCTGAGG 240
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Qy 567 TTTAACTTTGACTGCTATAGCAGAACCCGACAGGCCACAGATGGCTCCCTTGCTCCATT 626
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Qy 987 AAGTTTGAAGGCATCCCTCTGAGTCTTGGAGTGGATCTTTGCACCGGTCATCTTTTAT 1046
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QY      1887  AAGAAAAATTTTGA 1901
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ACCESSION  AY403532
VERSION     AY403532.1  GI:39759515
KEYWORDS   GSS.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
REFERENCE  1 (bases 1 to 1689)
AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
          Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
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          Adams,M.D. and Cargill,M.
          Inferring nonneutral evolution from human-chimp-mouse orthologous
          gene trios
          Science 302 (5652), 1960-1963 (2003)
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          2 (bases 1 to 1689)
          Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
          Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
          Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
          Adams,M.D. and Cargill,M.
          Direct Submission
          Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
          Rockville, MD 20850, USA
          This sequence was made by sequencing genomic exons and ordering
          them based on alignment.
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QY      327  TACACAGAAAAATCTTTGGGTCAACATTTGGCCTGTGCCGAGCGTCTGCTCTGCTTG 386
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QY      387  AATTTTACAGCAGCTGATCTCTGCTTCTGTGTGTCGCAATCTGCTGCTCTCTGAGG 446
Db      181  AATTTTAAACAGCATGATATCTGAATCTCTGTGTGTCGAAATCTGCTGTCTCTTGAGG 240

QY      447  GGCACCTGCTATTTTGAGCGGCACACTGAGAAAGCAATTTGGATCAACAACCTCACCTTC 506
Db      241  GGCACCTGCTATTTTGCAACGTTACACTGAGAAAGCCATTTGGATCAACAACCTCACCTTC 300

QY      507  CACAAGCTGGTGGCCATATATGATCTGCTCTACATACAGCTATTTCAATCTTGCACACCTG 566
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QY      627  CTCTCCAGCCTATCTCATGATGAGAAAAAGGGGGTTCTTTGGCTAAATCCCATCCAGTCC 686
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QY      687  CGAAAAACAGCAGTGGAGTATGTGAATTCACAGCGTTGCTGTTCTCACTCAGAGTATC 746
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QY      747  ATGACAATAGCCTTTGATTCTCATGGTAACTTCAGTACTAGTTCATCCCGAGAGATTAT 806
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QY      807  TTTGAAGTCTTCTGGTATACTCACCACTTTTATCTTCTATATCTCTTGGCTTAGGATT 866
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QY      927  CGCAAGTGTGCAGAGTCTTTTGAGATGTGGATGATCGTGACTCCCACTGTAGGCGCCT 986
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QY      987  AAGTTTGAAGGCGCATCCCTCGAGTCTTGGAAAGTGAATCTCTGACCGGTCACTCTTAT 1046
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Qy	1887	AAAGAAATTTTTGA	1901
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DEFINITION	IL3-CT0219-160200-063-E08	CT0219	Homo sapiens	cdna	mrna sequence.
ACCESSION	AW850622				
VERSION	AW850622.1	GI:7946139			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				

REFERENCE 1 (bases 1 to 668)

TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL PROC. NATL. ACAD. SCI. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil

taxid: 435-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (<http://www.ludwig.org.br/scripts/gethtml2.pl?t1=&t2=I13-CT0219-160>)
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            from ORSTES PCR (U.S. Letters Patent application No.
            196,716 - Ludwig Institute for Cancer Research) profiles
            into the pUC 18 vector. Reverse transcription of tissue
            mRNA and cDNA amplification were performed under low
            stringency conditions."

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ORIGIN

Query Match	25.2%;	Score 658.6;	DB 10;	Length 668;
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QY	1396	TGGCTGTGCTGGTTTGGAGCAGGAATTGGGGTCACCCCCTTTGCTTCTATCTTGAATCCA	1455	
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QY	1456	TCTGGTACAAATTCACGTGTGCAGACACACAACCTCAAAACAAAAAGATCTATTTCTTACT	1515	
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QY	1636	GGGACAGCAATATTTGTTGTCATCGACATTAACACTTTGACAAGGCCATGACATCGTGA	1695	
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LOCUS	IL3-CT0219-1911199-030-E11	CT0219	Homo sapiens	cdNA,	mRNA	sequence.
DEFINITION	AW377012					
ACCESSION	AW377012.1	GI:6881675				
VERSION	EST.					
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SOURCE	Homo sapiens					
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
REFERENCE	1 (bases 1 to 665)					
AUTHORS	HCGP	http://www.hcgp.org.br/ORESTES .				
TITLE	The FAPESP/LICR Human Cancer Genome Project					
JOURNAL	Unpublished (1999)					
COMMENT	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109. 4 andar. 01509-010. Sao Paulo-SP.					

Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL3&tl2=IL3-CT0219-191193-030-El1&t3=1999-11-19&t4=1)
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ORIGIN
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 Db 661 CAAA 664

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 AW604216.1 GI:7308957
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 Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 1 (bases 1 to 652)
 HGCP http://www.ludwig.org.br/ORESTES.
 AUTHORS
 The FAPESP/LICR Human Cancer Genome Project
 TITLE
 Unpublished (1999)
 JOURNAL
 COMMENT
 Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL3&tl2=IL3-CT0219-210100-059-F07&t3=2000-01-21&t4=1)
 Seq primer: puc 18 forward
 High quality sequence stop: 546.

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 /note="Organ: colon; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN
 Query Match 24.3%; Score 633.2; DB 10; Length 652;
 Best Local Similarity 98.9%; Pred. No. 7.4e-87;
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RESULT 7

AW850616

LOCUS IL3-CT0219-160200-063-C10 CT0219 Homo sapiens cDNA, mRNA sequence.

DEFINITION AW850616

ACCESSION AW850616.1 GI:7946133

VERSION

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS 1 (bases 1 to 618)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE 20202663

PUBMED 10737800

COMMENT Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=IL3-CT0219-160200-063-C10&t3=2000-02-16&t4=1)

Seq primer: puc 18 forward

High quality sequence stop: 565.

Location/Qualifiers

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from ORBESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 23.6%; Score 614.8; DB 10; Length 618; Best Local Similarity 99.7%; Pred. No. 4.8e-84; Matches 616; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1156 TCAGCATGGAAGTGGGCGAGTATATCTTTGTTAAATGCCCCCAATCTCTCTCGGAAT 1215

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QY 1216 GGATCTCTTTTACTTTTGACCTCTGCTCCAGAGGAAGATTTCTTCCATTCATATCCGAG 1275

Db 61 GGATCTCTTTTACTTTTGACCTCTGCTCCAGAGGAAGATTTCTTCCATTCATATCCGAG 120

QY 1276 CAGCAGGGGACTGGACAGAAATCTCATAGGGCTTTTCGAACCAACAATATTCACCAATTC 1335

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QY 1336 CAGGATTTGAAGTGGATGGTCCCTTTGGGCACAGCCAGTGGATGTTTCCAGTATGAAG 1395

Db 181 CAGGATTTGAAGTGGATGGTCCCTTTGGGCACAGCCAGTGGATGTTTCCAGTATGAAG 240

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QY 1576 AGGAGATGGAGGAATTAGGCAAAAGTGGGTTTCTTAACTACCGTCTCTTCTCACCGGAT 1635

Db 421 AGGAGATGGAGGAATTAGGCAAAAGTGGGTTTCTTAACTACCGTCTCTTCTCACCGGAT 480

QY 1636 GGACAGCAATATTTGGTTCATGCAGCATTAACCTTTTGACAAAGGCCACTGCATCGTGA 1695

Db 481 GGACAGCAATATTTGGTTCATGCAGCATTAACCTTTTGACAAAGGCCACTGCATCGTGA 540

QY 1696 CAGGTCTGAAACAGAAACCTCTTTGGGAGACCAATGTGGGACAAATGAGTTTCTACAA 1755

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RESULT 8

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LOCUS IL3-CT0219-221199-029-G09 CT0219 Homo sapiens cDNA, mRNA sequence.

DEFINITION AW752752

ACCESSION AW752752.1 GI:7667684

VERSION

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS 1 (bases 1 to 695)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and

Simpson A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE
20202663
PUBMED
10737800
COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL3&t2=IL3-CT0219-
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Seq primer: puc 18 forward
High quality sequence start: 21
High quality sequence stop: 618.

FEATURES

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/dev_stage="Adult"
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Smal; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No.
196,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."

ORIGIN

Query Match 23.6%; Score 614.6; DB 10; Length 695;
Best Local Similarity 91.4%; Pred. No. 4.8e-84;
Matches 684; Conservative 0; Mismatches 7; Indels 57; Gaps 1;
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Qy 1660 CAGATTAACTTTGACAAAGCCCACTGACATCGTGACAGGTCTGAAACAGAAAACCTCCT 1719
Db 515 CAGATTAACTTTGACAAAGCCCACTGACATCGTGACAGGTCTGAAACAGAAAACCTCCT 456
Qy 1720 TTGGGAGACCAATGTGGACAAATGTTTCTACAAATAGCTACCTCCACCCCAAGTCGTG 1779
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RESULT 9
AW604206 607 bp mRNA linear EST 23-MAR-2000
LOCUS IL3-CT0219-21C100-059-C11 CT0219 Homo sapiens cDNA, mRNA sequence.
DEFINITION
ACCESSION AW604206
VERSION AW604206.1 GI:7308947
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 607)
AUTHORS HCGP http://www.ludwig.org.br/ORESTES.
TITLE The FAPESP/LICR Human Cancer Genome Project
JOURNAL Unpublished (1999)
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL3&t2=IL3-CT0219-
210100-059-C11&t3=2000-01-21&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 606.

FEATURES

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/note="Organ: colon; Vector: puc18; Site 1: Smal; Site 2:
Smal; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No.
196,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."

ORIGIN

Query Match 23.2%; Score 605.4; DB 10; Length 607;
Best Local Similarity 99.8%; Pred. No. 1.3e-82;
Matches 606; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1156 TCACATGGAATGGGCGCATATATCTTTGTAATTCGCCCTCAATCTCTCTCTCGGAAT 1215
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 QY 1636 GGGACAGCAATATTTGTTGTCATGCAGCATTAACCTTTGACAGGCCACTGACATCGTA 1695
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RESULT 10

AW850625 618 bp mRNA linear EST 19-MAY-2000
 LOCUS IL3-CT0219-160200-063-G06 CT0219 Homo sapiens cDNA, mRNA sequence.
 DEFINITION AW850625
 ACCESSION AW850625.1 GI:7946142
 VERSION EST.
 KEYWORDS Homo sapiens (human)

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 618)
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
 Nagai, M.A., da Silva W. Jr., Zago, M.A., Bordin, S., Costa, F.,
 Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
 Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V.,
 O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
 Simpson, A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags

TITLE

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 20202663
 10737800
 Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research

JOURNAL

MEDLINE
 PUBMED
 COMMENT
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=st2-IL3-CT0219-160
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 Seq primer: puc 18 forward
 High quality sequence stop: 617.
 Location/Qualifiers
 1. 618

FEATURES

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 SmaI; A mini-library was made by cloning products derived
 from ORESTES PCR (U.S. Letters Patent application No.
 196,716 - Ludwig Institute for Cancer Research) profiles
 into the pUC 18 vector. Reverse transcription of tissue
 mRNA and cDNA amplification were performed under low
 stringency conditions."

ORIGIN

Query Match 23.1%; Score 601.8; DB 10; Length 618;
 Best Local Similarity 99.4%; Pred. No. 4.5e-82;
 Matches 614; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
 QY 1156 TCAGCATGGAAGTGGGGCAGTATATCTTGTAAAT-GGCCCTCAATCTCTCTCCCTGGAA 1214
 Db 1 TCAGCATGGAAGTGGGGCAGTATATCTTGTAAATAGCCCTCAATCTCTCCCTGGAA 60
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 QY 1695 ACAGGTCTGAAACAGAAAACCTCTTTGGGAGACCAATGTGGGACAAATGAGTTTTCTACA 1754
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 Db 601 ATAGTACTCTCCACCCC 618

RESULT 11

AW604209

LOCUS AW604209 605 bp mRNA linear EST 23-MAR-2000
 DEFINITION IL3-CT0219-210100-059-E04 CT0219 Homo sapiens cDNA, mRNA sequence.
 ACCESSION AW604209
 VERSION AW604209.1 GI:7308950
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 605)
 HCSP <http://www.ludwig.org.br/ORESTES>.
 The FAPESP/LICR Human Cancer Genome Project
 Unpublished (1999)
 CONTACT: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL3&t2=IL3-CT0219-210100-059-E04&t3=2000-01-21&t4=1>)
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 High quality sequence stop: 552.
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 SmI; A mini-library was made by cloning products derived
 from ORESTES PCR (U.S. Letters Patent application No.
 196,716 - Ludwig Institute for Cancer Research) profiles
 into the pUC 18 vector. Reverse transcription of tissue
 mRNA and cDNA amplification were performed under low
 stringency conditions."
 FEATURES
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 SmI; A mini-library was made by cloning products derived
 from ORESTES PCR (U.S. Letters Patent application No.
 196,716 - Ludwig Institute for Cancer Research) profiles
 into the pUC 18 vector. Reverse transcription of tissue
 mRNA and cDNA amplification were performed under low
 stringency conditions."
 ORIGIN
 Query Match 22.9%; Score 597.2; DB 10; Length 605;
 Best Local Similarity 99.0%; Pred No. 2.3e-81;
 Matches 599; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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 DB 1 TCAGCATGGAAGTGGGCGAGTATATCTTTGTTAAATGCGCCCTCAATCTCTCTCTGGAAAT 60
 QY 1216 GGCATCTTTTACTTTGACCTCTGCTCCAGGAGAGATTTCTTCCATTATATCCGAG 1275
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 DB 181 CCAGGANTGAAGTGAATGCTCCCTTTGGCAGCAGGAGAGATTTTCCAGTAGAAG 240
 QY 1396 TGGCTGTCTGTTGGAGCAGGAATGGGGTCAACCCCTTGTCTTCTATCTTGAATCCA 1455
 DB 241 TGGCTGTCTGTTGGAGCAGGAATGGGGTCAACCCCTTGTCTTCTATCTTGAATCCA 300
 QY 1456 TCTGTACAAATTCAGATGTGAGACCAACAACCTCAAAACAAAAAGATCTATTTCTACT 1515
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 QY 1516 GGATCTCAGGAGACAGGTGCTTTTCTGTTCAACACCTGTGTGATTCCTCCCTGGAAC 1575
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Db 361 GGATCTCGAGGAGACAGGTGCCTTTTCTCGTGTTCACAAACCTCTTGGCTTCCCTCGGAAC 420
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 LOCUS AK053920
 DEFINITION Mus musculus 2 days pregnant adult female oviduct cDNA, RIKEN
 full-length enriched library, clone E230001H16 product:cytochrome
 b-245, beta polypeptide, full insert sequence.
 ACCESSION AK053920
 VERSION AK053920.1 GI:26343872
 KEYWORDS HTC; CAP trapper.
 SOURCE Mus musculus (house mouse)
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 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1
 Carninci P. and Hayashizaki Y.
 High-efficiency full-length cDNA cloning
 Meth. Enzymol. 303, 19-44 (1999)
 JOURNAL 99279253
 MEDLINE 10349636
 PUBMED 10349636
 REFERENCE 2
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 Itoh M., Konno H., Okazaki Y., Muramatsu M. and Hayashizaki Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes
 Genome Res. 10 (10), 1617-1630 (2000)
 JOURNAL 20499374
 MEDLINE 11042159
 PUBMED 11042159
 REFERENCE 3
 Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 Konno H., Akiyama J., Nishi K., Kitsuina T., Tashiro H., Itoh M.,
 Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
 Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 Okazaki Y., Muramatsu M., Inoue Y., Kita A. and Hayashizaki Y.
 RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multipillar sequencer
 Genome Res. 10 (11), 1757-1771 (2000)
 JOURNAL 20530913
 MEDLINE 11076861
 PUBMED 11076861
 REFERENCE 4
 The RIKEN Genome Exploration Research Group Phase II Team and the
 FANTOM Consortium.
 Functional annotation of a full-length mouse cDNA collection
 Nature 409, 685-690 (2001)
 JOURNAL 11076861
 MEDLINE 11076861
 PUBMED 11076861
 REFERENCE 5
 The FANTOM Consortium and the RIKEN Genome Exploration Research
 Group Phase I & II Team.
 Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)
 JOURNAL 11076861
 MEDLINE 11076861
 PUBMED 11076861
 REFERENCE 6
 (bases 1 to 3242)
 Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 Itoh M., Konno H., Okazaki Y., Muramatsu M. and Hayashizaki Y.

Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
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Okazaki,Y., Saito,H., Saitoh,K., Sakai,C., Sakai,K., Sakazume,N.,
Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
Muratsu,M. and Hayashizaki,Y.
Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/
URL:http://location.qualifiers

FEATURES
source

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ORIGIN

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199 AATTTTCACTGTATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 258
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 ACCESSION AW376980
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 HCGP <http://www.ludwig.org.br/ORESTES>.
 TITLE The FAPESP/LICR Human Cancer Genome Project
 JOURNAL Unpublished (1999)
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
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from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

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 1 (bases 1 to 4000)
 Direct Submission
 TITLE Strausberg, R.
 JOURNAL
 AUTHORS
 REFERENCE
 REMARK
 COMMENT NIH-MGC Project URL: <http://mgc.mci.nih.gov>
 Contact: MGC help desk

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 ORGANISM
 Homo sapiens

REFERENCE
 AUTHORS
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Mateukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 20202663
 10737800
 Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=st2-IL3-CT0219-160
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ORIGIN
 Query Match 22.2%; Score 579.8; DB 10; Length 583;
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